GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 90 Seconds
(without alignments)
139.506 Million cell updates/sec

Title: US-10-802-574-3
Perfect score: 172
Sequence: 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	169	98.3	37	2	AAR86822	Aar86822 VAMP isof
2	169	98.3	40	4	AAB50301	Aab50301 VAMP2 pep
3	169	98.3	40	4	AAB48582	Aab48582 VAMP2 pep
4	169	98.3	42	5	AAO15163	Aao15163 Clostridi
5	169	98.3	54	3	AAB39482	Aab39482 Gene 49 h
6	169	98.3	62	2	AAR86821	Aar86821 VAMP isof
7	169	98.3	115	7	ADE57598	Ade57598 Human Pro
8	169	98.3	115	7	ADE57612	Ade57612 Rat Prote
9	169	98.3	115	7	ADE60831	Ade60831 Human Pro
10	169	98.3	115	7	ADE57606	Ade57606 Human Pro
11	169	98.3	115	7	ADE60829	Ade60829 Rat Prote
12	169	98.3	115	7	ADE57600	Ade57600 Rat Prote
13	169	98.3	115	7	ADE57604	Ade57604 Rat Prote
14	169	98.3	115	7	ADE57596	Ade57596 Rat Prote
15	169	98.3	115	7	ADE57602	Ade57602 Human Pro
16	169	98.3	115	7	ADE57610	Ade57610 Human Pro
17	169	98.3	115	7	ADE57592	Ade57592 Rat Prote
18	169	98.3	115	7	ADE57594	Ade57594 Human Pro
19	169	98.3	115	7	ADE57614	Ade57614 Human Pro
20	169	98.3	115	7	ADE57608	Ade57608 Rat Prote
21	169	98.3	116	2	AAW30104	Aaw30104 Vesicle-a
22	169	98.3	116	2	AAW43425	Aaw43425 Rat vesic
23	169	98.3	116	3	AAY88243	Aay88243 Bovine sy
24	169	98.3	116	5	ABP43681	Abp43681 VAMP-2 se
25	169	98.3	116	6	ABP76220	Abp76220 Human GEN
26	169	98.3	116	6	AAE36664	Aae36664 Human VAM
27	169	98.3	116	7	ABW01719	Abw01719 Bovine VA
28	169	98.3	116	7	ABW01718	Abw01718 Mouse VAM
29	169	98.3	116	7	ABW01705	Abw01705 Human VAM
30	169	98.3	116	7	ADG89011	Adg89011 Bovine sy
31	169	98.3	116	8	ADM97006	Adm97006 Mouse VAM
32	169	98.3	116	8	ADM97007	Adm97007 Bovine VA
33	169	98.3	116	8	ADM97005	Adm97005 Human VAM
34	169	98.3	368	3	AAY43843	Aay43843 Amino aci
35	169	98.3	368	7	ADF90403	Adf90403 Rat VAMP-
36	169	98.3	608	3	AAY43845	Aay43845 Amino aci
37	169	98.3	609	7	ADF90406	Adf90406 Rat VAMP-
38	167	97.1	35	5	AAO15157	Aao15157 Clostridi
39	167	97.1	82	3	AAY88244	Aay88244 Xenopus s
40	167	97.1	82	7	ADG89012	Adg89012 Xenopus s
41	167	97.1	114	7	ABW01720	Abw01720 Frog VAMP
42	167	97.1	114	8	ADM97008	Adm97008 Frog VAMP
43	164	95.3	35	2	AAR86824	Aar86824 VAMP isof
44	164	95.3	100	2	AAW04182	Aaw04182 Cellubrev
45	164	95.3	100	3	AAY88240	Aay88240 Human cel

ALIGNMENTS

RESULT 1
AAR86822
ID AAR86822 standard; peptide; 37 AA.
XX
AC AAR86822;
XX
DT 15-AUG-1996 (first entry)
XX
DE VAMP isoform-1 residues 60-94 (plus N- and C-terminal cysteines).
XX
KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;
KW antibody; detection; assay.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label= N-terminal Cysteine
FT /note= "may be present to attach peptide to solid-phase"
FT Peptide 2. .36
FT /note= "VAMP isoform-1 residues 60-94"
FT Misc-difference 37
FT /label= C-terminal cysteine
FT /note= "may be present to attach to peptide to solid-
FT phase"
XX
PN WO9533850-A1.
XX
PD 14-DEC-1995.
XX
PF 02-JUN-1995; 95WO-GB001279.
XX
PR 03-JUN-1994; 94GB-00011138.
XX
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX
PI Shone CC, Hallis B, James BAF, Quinn CP;
XX
DR WPI; 1996-040249/04.
XX
PT Assay for botulinum or tetanus toxin - by combining test cpd. with
PT substrate which is cleaved by the toxin, and antibody specific for the
PT cleaved but not uncleaved substrate.
XX
PS Example 1; Page 28-29; 48pp; English.
XX

CC The botulinum neurotoxins possess highly specific zinc-endopeptidase
CC activities within their light sub-units. Depending on the neurotoxin type
CC these act to cleave small proteins within the nerve cell which are
CC involved in neurotransmitter release. Antibodies are used in assays which
CC detect cleaved but not uncleaved substrate. An assay for botulinum type B
CC uses the present sequence as a substrate. It is VAMP (vesicle- associated
CC membrane protein) isoform-1, residues 60-94. The VAMP peptide can be
CC attached by a C- or N-terminal cysteine to a solid phase
XX
SQ Sequence 37 AA;

Query Match 98.3%; Score 169; DB 2; Length 37;
Best Local Similarity 94.3%; Pred. No. 6.6e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 2 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 36

RESULT 2
AAB50301
ID AAB50301 standard; peptide; 40 AA.
XX
AC AAB50301;
XX
DT 08-MAR-2001 (first entry)
XX
DE VAMP2 peptide.
XX
KW VAMP2; antibacterial; Botulinum toxin inhibitor; BttxB; previn;
KW tetanus neurotoxin; buforinin.
XX
OS Unidentified.
XX
PN WO200069891-A2.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-US013215.
XX
PR 17-MAY-1999; 99US-0134446P.
XX
PA (USSA) US DEPT OF THE ARMY.
XX
PI Gordon RK, Moorad DR, Doctor BP, Garcia GE;
XX
DR WPI; 2001-025001/03.
XX
PT Novel Previn compounds useful for inhibiting the protease activity of
PT Botulinum B and tetanus toxins.
XX
PS Disclosure; Page 5; 47pp; English.
XX
CC The present sequence was investigated in the search for Botulinum toxin
CC inhibitors (BttxB). Previn compounds which inhibit the enzymatic activity
CC of BttxB and tetanus neurotoxins were isolated. Previns may be used to
CC construct compounds such as buforinins
XX
SQ Sequence 40 AA;

Query Match 98.3%; Score 169; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 7.2e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40

RESULT 3
AAB48582
ID AAB48582 standard; peptide; 40 AA.
XX
AC AAB48582;
XX
DT 08-MAR-2001 (first entry)
XX
DE VAMP2 peptide.
XX
KW Buforin; Botulinum toxin B; BttxB; Tetanus neurotoxin; endoprotease;
KW antibacterial; VAMP2; synaptobrevin.
XX
OS Unidentified.
XX
PN WO200069895-A2.
XX
PD 23-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US012909.
XX
PR 14-MAY-1999; 99US-0134216P.
XX
PA (USSA) US DEPT OF THE ARMY.
XX
PI Garcia GE, Gordon RK, Moorad DR, Doctor BP;
XX
DR WPI; 2001-102250/11.
XX
PT Novel peptides capable of inhibiting the enzymatic activity of Botulinum
PT toxin B, and Tetanus neurotoxins useful for preventing or treating toxic
PT poisoning such as Botulinum toxin and tetanus poisoning.
XX
PS Disclosure; Page 5; 47pp; English.
XX
CC The present sequence is one of a number of peptide or peptide-like
CC compounds, designated buforins, which inhibit the enzymatic activity of
CC Botulinum toxin B (BttxB) and Tetanus neurotoxins. The buforins are
CC useful for treating Botulinum or tetanus intoxication by administering a
CC composition comprising a buforin to the subject prior to the contact with
CC BttxB or tetanus intoxication. Antibodies specific for buforins are
CC useful for detecting buforins by forming immunocomplexes. The buforins
CC have improved circulatory half-life, solubility, resistance to
CC degradation and interaction with the active site of the toxin
XX
SQ Sequence 40 AA;

Query Match 98.3%; Score 169; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 7.2e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40

RESULT 4
AAO15163
ID AAO15163 standard; peptide; 42 AA.
XX
AC AAO15163;
XX
DT 02-SEP-2002 (first entry)
XX
DE Clostridial neurotoxin protease substrate peptide 2.
XX
KW Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
KW fluorescence resonant energy transfer assay; quenched-signal;
KW clostridial neurotoxin detection; food.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-fluoresceinyl-glycine"
FT Cleavage-site 20. .21

FT /note= "The peptide is cleaved between these two residues
FT by the clostridial neurotoxin"
XX
PN WO200225284-A2.
XX
PD 28-MAR-2002.
XX
PF 25-SEP-2001; 2001WO-US030188.
XX
PR 25-SEP-2000; 2000US-0235050P.
XX
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Schmidt JJ, Stafford RG;
XX
DR WPI; 2002-499829/53.
XX
PT Substrate useful in e.g. an assay for the protease activity of
PT clostridial neurotoxin, comprises modified peptide or protein.
XX
PS Claim 24; Page 15; 48pp; English.
XX
CC The invention comprises clostridial neurotoxin substrate peptides which
CC can serve as fluorescence resonant energy transfer assay (FRET) or
CC quenched-signal substrates in assays for the proteolytic activities of
CC clostridial neurotoxins. The invention further comprises Clostridium
CC botulinum neurotoxin substrate peptides that can serve as immobilised
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
CC activities of clostridial neurotoxins. The clostridial (including the
CC Clostridium botulinum) neurotoxin substrate peptides are useful for
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
CC or an environmental sample). The present amino acid sequence represents a
CC clostridial neurotoxin substrate peptide of the invention
XX
SQ Sequence 42 AA;

Query Match 98.3%; Score 169; DB 5; Length 42;
Best Local Similarity 94.3%; Pred. No. 7.6e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38

RESULT 5
AAB39482
ID AAB39482 standard; protein; 54 AA.
XX
AC AAB39482;
XX
DT 02-FEB-2001 (first entry)
XX
DE Gene 49 human secreted protein homologous amino acid sequence #141.
XX
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; gene therapy;
KW food additive; preservative; chromosome identification; cancer;
KW female reproductive system disorder; immune disorder; wound healing;
KW cardiovascular disorder; neurological disease; infectious disease;
KW infection.
XX
OS Bos taurus.
XX
PN WO200058340-A2.
XX
PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US007724.
XX
PR 26-MAR-1999; 99US-0126510P
PR 07-JAN-2000; 2000US-0174850P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-594638/56.
XX
PT Fifty nucleic acid molecules encoding human secreted proteins, useful in
PT the prevention, treatment and diagnosis of cancer, immune disorders,
PT cardiovascular disorders and neurological diseases.
XX
PS Disclosure; Page 390; 391pp; English.
XX
CC The polynucleotide sequences given in AAC74337 to AAC74386 encode the
CC human secreted proteins given in AAB39402 to AAB39451. AAB39452 to
CC AAB39484 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
CC antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
CC vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and
CC cardiant. The polynucleotides and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides
CC can also be used as a food additive or preservative to increase or
CC decrease storage capabilities. The polynucleotide are useful for
CC chromosome identification. They are also useful as probes for diagnosing
CC a disorder related to the female reproductive system, particularly breast
CC and/or ovary cancer. They are also useful in the gene therapy of breast
CC and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies,
CC agonists and antagonists are useful in the diagnosis, treatment and
CC prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular
CC disorders; (d) wound healing; (e) neurological diseases; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 54 AA;

Query Match 98.3%; Score 169; DB 3; Length 54;
Best Local Similarity 94.3%; Pred. No. 1e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 20 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 54

RESULT 6
AAR86821
ID AAR86821 standard; peptide; 62 AA.
XX
AC AAR86821;
XX
DT 15-AUG-1996 (first entry)
XX
DE VAMP isoform-1 residues 33-94.
XX
KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;
KW antibody; detection; assay.
XX
OS Synthetic.
XX
PN WO9533850-A1.
XX
PD 14-DEC-1995.
XX
PF 02-JUN-1995; 95WO-GB001279.
XX
PR 03-JUN-1994; 94GB-00011138.

XX
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX
PI Shone CC, Hallis B, James BAF, Quinn CP;
XX
DR WPI; 1996-040249/04.
XX
PT Assay for botulinum or tetanus toxin - by combining test cpd. with
PT substrate which is cleaved by the toxin, and antibody specific for the
PT cleaved but not uncleaved substrate.
XX
PS Example 3; Page 28; 48pp; English.
XX
CC The botulinum neurotoxins possess highly specific zinc-endopeptidase
CC activities within their light sub-units. Depending on the neurotoxin type
CC these act to cleave small proteins within the nerve cell which are
CC involved in neurotransmitter release. Antibodies are used in assays which
CC detect cleaved but not uncleaved substrate. Tetanus toxin cleaves the
CC protein VAMP (vesicle-associated membrane protein) at an identical site
CC to that of botulinum toxin type B (BoNT/B). The specificities of the
CC endopeptidase activities of the two toxins however differ in the minimum
CC peptide substrate size required for cleavage. While BoNT/B requires
CC peptide substrates of 30-35 residues in length for optimal cleavage, the
CC requirement for tetanus toxin is peptide substrates of >50 residues in
CC length. The present sequence, VAMP isoform-1 residues 33-94, is a
CC suitable substrate for tetanus toxin
XX
SQ Sequence 62 AA;

Query Match 98.3%; Score 169; DB 2; Length 62;
Best Local Similarity 94.3%; Pred. No. 1.2e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         28 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 62
```

RESULT 7
ADE57598
ID ADE57598 standard; protein; 115 AA.
XX
AC ADE57598;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 3460.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
```

RESULT 8
ADE57612
ID ADE57612 standard; protein; 115 AA.
XX
AC ADE57612;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3474.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;

XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 9
ADE60831
ID ADE60831 standard; protein; 115 AA.
XX
AC ADE60831;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 6743.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 10
ADE57606
ID ADE57606 standard; protein; 115 AA.
XX
AC ADE57606;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 3468.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 11
ADE60829
ID ADE60829 standard; protein; 115 AA.
XX
AC ADE60829;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 6741.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 12
ADE57600
ID ADE57600 standard; protein; 115 AA.
XX
AC ADE57600;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3462.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

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  Query Match             98.3%;  Score 169;  DB 7;  Length 115;
  Best Local Similarity   94.3%;  Pred. No. 2.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
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RESULT 13
ADE57604
ID ADE57604 standard; protein; 115 AA.
XX
AC ADE57604;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3466.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

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  Query Match             98.3%;  Score 169;  DB 7;  Length 115;
  Best Local Similarity   94.3%;  Pred. No. 2.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
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RESULT 14
ADE57596
ID ADE57596 standard; protein; 115 AA.

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AC ADE57596;
XX
DT 29-JAN-2004 (first entry)
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DE Rat Protein Q64357, SEQ ID NO 3458.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
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CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 15
ADE57602
ID ADE57602 standard; protein; 115 AA.
XX
AC ADE57602;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 3464.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
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CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
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Job time : 92 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 23.4375 Seconds
(without alignments)
99.035 Million cell updates/sec

Title: US-10-802-574-3
Perfect score: 172
Sequence: 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	169	98.3	35	2	US-08-760-001-11	Sequence 11, Appl
3	169	98.3	35	3	US-09-015-960-9	Sequence 9, Appli
4	169	98.3	35	3	US-09-015-960-11	Sequence 11, Appl
5	169	98.3	35	3	US-09-534-572-9	Sequence 9, Appli
6	169	98.3	35	3	US-09-534-572-11	Sequence 11, Appl
7	169	98.3	40	4	US-09-570-022-16	Sequence 16, Appl
8	169	98.3	40	4	US-09-570-023-8	Sequence 8, Appli
9	169	98.3	42	4	US-09-962-360B-9	Sequence 9, Appli
10	169	98.3	62	2	US-08-760-001-8	Sequence 8, Appli
11	169	98.3	62	3	US-09-015-960-8	Sequence 8, Appli
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14	169	98.3	116	1	US-08-409-373B-4	Sequence 4, Appli
15	169	98.3	116	1	US-08-393-985-16	Sequence 16, Appl
16	169	98.3	116	3	US-08-621-018B-10	Sequence 10, Appl
17	169	98.3	116	3	US-08-819-286-2	Sequence 2, Appli
18	169	98.3	116	4	US-09-483-665-10	Sequence 10, Appl
19	168	97.7	35	4	US-09-962-360B-3	Sequence 3, Appli
20	167	97.1	82	3	US-08-621-018B-11	Sequence 11, Appl
21	167	97.1	82	4	US-09-483-665-11	Sequence 11, Appl
22	164	95.3	100	3	US-08-621-018B-6	Sequence 6, Appli
23	164	95.3	100	4	US-09-483-665-6	Sequence 6, Appli
24	164	95.3	103	1	US-08-409-373B-3	Sequence 3, Appli
25	164	95.3	103	1	US-08-409-373B-3	Sequence 3, Appli
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30	164	95.3	350	4	US-09-513-783A-30	Sequence 30, Appl
31	164	95.3	350	4	US-09-430-656-28	Sequence 28, Appl
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34	105	61.0	56	3	US-08-819-286-5	Sequence 5, Appli
35	92	53.5	94	4	US-09-621-976-6274	Sequence 6274, Ap
36	85	49.4	71	4	US-09-621-976-5656	Sequence 5656, Ap
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39	85	49.4	102	1	US-08-409-373B-2	Sequence 2, Appli
40	85	49.4	102	3	US-08-621-018B-2	Sequence 2, Appli
41	85	49.4	102	4	US-09-483-665-2	Sequence 2, Appli
42	81	47.1	20	3	US-08-819-286-13	Sequence 13, Appl
43	74	43.0	141	3	US-08-621-018B-8	Sequence 8, Appli
44	74	43.0	141	4	US-09-483-665-8	Sequence 8, Appli
45	68	39.5	46	4	US-09-962-360B-10	Sequence 10, Appl

ALIGNMENTS

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; Patent No. 5962637
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/760,001
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-760-001-9

  Query Match           98.3%;  Score 169;  DB 2;  Length 35;
  Best Local Similarity  94.3%;  Pred. No. 6e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db          1 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 35


RESULT 2
US-08-760-001-11
; Sequence 11, Application US/08760001
; Patent No. 5962637
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/760,001
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-760-001-11

  Query Match             98.3%;  Score 169;  DB 2;  Length 35;
  Best Local Similarity   94.3%;  Pred. No. 6e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db          1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35


RESULT 3
US-09-015-960-9
; Sequence 9, Application US/09015960
; Patent No. 6043042
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/015,960
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-015-960-9

  Query Match             98.3%;  Score 169;  DB 3;  Length 35;
  Best Local Similarity   94.3%;  Pred. No. 6e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db          1 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 35


RESULT 4
US-09-015-960-11
; Sequence 11, Application US/09015960
; Patent No. 6043042
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/015,960
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
```

; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-015-960-11

Query Match 98.3%; Score 169; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 6e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db 1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35

RESULT 5
US-09-534-572-9
; Sequence 9, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-534-572-9

Query Match 98.3%; Score 169; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 6e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| ||||||||||||||||
Db 1 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 35

RESULT 6
US-09-534-572-11
; Sequence 11, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-534-572-11

Query Match 98.3%; Score 169; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 6e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db 1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35

```
RESULT 7
US-09-570-022-16
; Sequence 16, Application US/09570022
; Patent No. 6573244
; GENERAL INFORMATION:
;  APPLICANT: GORDON, RICHARD K.
;  APPLICANT:  MOORAD, DEBORAH R.
;  APPLICANT:  DOCTOR, BHUPENDRA P.
;  APPLICANT:  GARCIA, GREGORY E.
;  TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
;  TITLE OF INVENTION:  FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
;  FILE REFERENCE: 38644-170531
;  CURRENT APPLICATION NUMBER: US/09/570,022
;  CURRENT FILING DATE:  2000-05-12
;  PRIOR APPLICATION NUMBER: 60/134,446
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-570-022-16

  Query Match             98.3%;  Score 169;  DB 4;  Length 40;
  Best Local Similarity   94.3%;  Pred. No. 7e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db          6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40


RESULT 8
US-09-570-023-8
; Sequence 8, Application US/09570023
; Patent No. 6713444
; GENERAL INFORMATION:
;  APPLICANT: GARCIA, GREGORY E.
;  APPLICANT:  GORDON, RICHARD K.
;  APPLICANT:  MOORAD, DEBBIE R.
;  APPLICANT:  DOCTOR, BHUPENDRA P.
;  TITLE OF INVENTION: BUFORIN I AS A SPECIFIC INHIBITOR AND THERAPEUTIC AGENT
;  TITLE OF INVENTION:  FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
;  FILE REFERENCE: 37833-20004.00
;  CURRENT APPLICATION NUMBER: US/09/570,023
;  CURRENT FILING DATE:  2000-05-12
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: VAMP2
US-09-570-023-8

  Query Match             98.3%;  Score 169;  DB 4;  Length 40;
  Best Local Similarity   94.3%;  Pred. No. 7e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db          6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40


RESULT 9
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
;   /9
;  APPLICANT: Schmidt, James J.
;  APPLICANT:  Stafford, Robert G.
;  TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
;  TITLE OF INVENTION:  Neurotoxins
;  FILE REFERENCE: 003/224/SAP
;  CURRENT APPLICATION NUMBER: US/09/962,360B
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/235,050
;  PRIOR FILING DATE: 2001-09-25
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
;   LENGTH: 42
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1
;   OTHER INFORMATION: Xaa at 1 is N-flurescein-glycine
US-09-962-360B-9

  Query Match             98.3%;  Score 169;  DB 4;  Length 42;
  Best Local Similarity   94.3%;  Pred. No. 7.4e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38


RESULT 10
US-08-760-001-8
; Sequence 8, Application US/08760001
; Patent No. 5962637
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/760,001
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 amino acids
;      TYPE:  amino acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-760-001-8

  Query Match             98.3%;  Score 169;  DB 2;  Length 62;
  Best Local Similarity   94.3%;  Pred. No. 1.1e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         28 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 62


RESULT 11
US-09-015-960-8
; Sequence 8, Application US/09015960
; Patent No. 6043042
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/015,960
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-015-960-8

  Query Match             98.3%;  Score 169;  DB 3;  Length 62;
  Best Local Similarity   94.3%;  Pred. No. 1.1e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         28 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 62


RESULT 12
US-09-534-572-8
; Sequence 8, Application US/09534572
; Patent No. 6337386
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/534,572
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/015,960
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:  30-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-534-572-8

  Query Match             98.3%;  Score 169;  DB 3;  Length 62;
  Best Local Similarity   94.3%;  Pred. No. 1.1e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db         28 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 62


RESULT 13
US-08-409-373B-4
; Sequence 4, Application US/08409373B
; Patent No. 5585240
;  GENERAL INFORMATION:
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  CELLUBREVIN HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
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;     ZIP:  94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/409,373B
;     FILING DATE:  23-MAR-1995
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Luther, Barbara J
;     REGISTRATION NUMBER:  33,954
;     REFERENCE/DOCKET NUMBER:  PF-0029 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415-855-0555
;     TELEFAX:  415-852-0195
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  116 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   IMMEDIATE SOURCE:
;     LIBRARY:  GenBank
;     CLONE:  X76199
US-08-409-373B-4

  Query Match             98.3%;  Score 169;  DB 1;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 2.3e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 14
US-08-409-373B-4
; Sequence 4, Application US/08409373B
; Patent No. 5650280
; Patent No. 5650280 5585240
; GENERAL INFORMATION:
;   APPLICANT:  Stuart, Susan G.
;   APPLICANT:  Hawkins, Phillip R.
;   APPLICANT:  Seilhamer, Jeffrey J.
;   TITLE OF INVENTION:  CELLUBREVIN HOMOLOG
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;     STREET:  3174 Porter Drive
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  U.S.
;     ZIP:  94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/409,373B
;     FILING DATE:  23-MAR-1995
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Luther, Barbara J
;     REGISTRATION NUMBER:  33,954
;     REFERENCE/DOCKET NUMBER:  PF-0029 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415-855-0555
;     TELEFAX:  415-852-0195
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  116 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   IMMEDIATE SOURCE:
;     LIBRARY:  GenBank
;     CLONE:  X76199
US-08-409-373B-4

  Query Match             98.3%;  Score 169;  DB 1;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 2.3e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 15
US-08-393-985-16
; Sequence 16, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
;   APPLICANT:  Scheller, Richard H.
;   TITLE OF INVENTION:  Methods and Compositions for Modulation
;   TITLE OF INVENTION:  of Vesicular Release
;   NUMBER OF SEQUENCES:  35
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Dehlinger & Associates
;     STREET:  350 Cambridge Avenue, Suite 250
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94306
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/393,985
;     FILING DATE:
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Sholtz, Charles K.
;     REGISTRATION NUMBER:  38,615
;     REFERENCE/DOCKET NUMBER:  8600-0152
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 324-0880
;     TELEFAX:  (415) 324-0960
; INFORMATION FOR SEQ ID NO:  16:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  116 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-393-985-16

  Query Match             98.3%;  Score 169;  DB 1;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 2.3e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


Search completed:  November  1, 2004, 18:19:41
Job time :  24.4375 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 69.0625 Seconds
(without alignments)
164.308 Million cell updates/sec

Title: US-10-802-574-3
Perfect score: 172
Sequence: 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	169	98.3	42	10	US-09-962-360B-9	Sequence 9, Appli
2	169	98.3	116	10	US-09-942-024-4	Sequence 4, Appli
3	169	98.3	116	10	US-09-942-024-17	Sequence 17, Appl
4	169	98.3	116	10	US-09-942-024-18	Sequence 18, Appl
5	169	98.3	116	10	US-09-942-098-4	Sequence 4, Appli
6	169	98.3	116	10	US-09-942-098-17	Sequence 17, Appl
7	169	98.3	116	10	US-09-942-098-18	Sequence 18, Appl
8	169	98.3	116	14	US-10-357-028-10	Sequence 10, Appl
9	169	98.3	116	15	US-10-261-161-11	Sequence 11, Appl
10	169	98.3	116	15	US-10-261-161-12	Sequence 12, Appl
11	169	98.3	116	15	US-10-261-161-13	Sequence 13, Appl
12	169	98.3	607	10	US-09-293-670-55	Sequence 55, Appl
13	168	97.7	35	10	US-09-962-360B-3	Sequence 3, Appli
14	167	97.1	82	14	US-10-357-028-11	Sequence 11, Appl
15	167	97.1	114	10	US-09-942-024-19	Sequence 19, Appl
16	167	97.1	114	10	US-09-942-098-19	Sequence 19, Appl
17	167	97.1	114	15	US-10-261-161-14	Sequence 14, Appl
18	164	95.3	100	14	US-10-357-028-6	Sequence 6, Appli
19	164	95.3	103	14	US-10-357-028-9	Sequence 9, Appli
20	164	95.3	117	16	US-10-467-595-27	Sequence 27, Appl
21	164	95.3	118	10	US-09-942-024-96	Sequence 96, Appl
22	164	95.3	118	10	US-09-942-098-96	Sequence 96, Appl
23	164	95.3	118	15	US-10-261-161-10	Sequence 10, Appl
24	164	95.3	347	14	US-10-100-957A-28	Sequence 28, Appl
25	164	95.3	350	14	US-10-100-957A-30	Sequence 30, Appl
26	164	95.3	365	10	US-09-293-670-52	Sequence 52, Appl
27	162	94.2	35	10	US-09-962-360B-4	Sequence 4, Appli
28	152	88.4	109	14	US-10-369-493-6364	Sequence 6364, Ap
29	149	86.6	40	10	US-09-942-024-57	Sequence 57, Appl
30	149	86.6	40	10	US-09-942-024-58	Sequence 58, Appl
31	149	86.6	40	10	US-09-942-024-60	Sequence 60, Appl
32	149	86.6	40	10	US-09-942-024-61	Sequence 61, Appl
33	149	86.6	40	10	US-09-942-024-65	Sequence 65, Appl
34	149	86.6	40	10	US-09-942-098-57	Sequence 57, Appl
35	149	86.6	40	10	US-09-942-098-58	Sequence 58, Appl
36	149	86.6	40	10	US-09-942-098-60	Sequence 60, Appl
37	149	86.6	40	10	US-09-942-098-61	Sequence 61, Appl
38	149	86.6	40	10	US-09-942-098-65	Sequence 65, Appl
39	149	86.6	40	15	US-10-261-161-82	Sequence 82, Appl
40	149	86.6	40	15	US-10-261-161-83	Sequence 83, Appl
41	149	86.6	40	15	US-10-261-161-85	Sequence 85, Appl
42	149	86.6	40	15	US-10-261-161-86	Sequence 86, Appl
43	149	86.6	40	15	US-10-261-161-90	Sequence 90, Appl
44	145	84.3	104	10	US-09-942-024-20	Sequence 20, Appl
45	145	84.3	104	10	US-09-942-098-20	Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
;    /9
;  APPLICANT: Schmidt, James J.
;  APPLICANT:  Stafford, Robert G.
;  TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
;  TITLE OF INVENTION:  Neurotoxins
;  FILE REFERENCE: 003/224/SAP
;  CURRENT APPLICATION NUMBER: US/09/962,360B
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/235,050
;  PRIOR FILING DATE: 2001-09-25
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
;   LENGTH: 42
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1
;   OTHER INFORMATION: Xaa at 1 is N-flureseinyl-glycine
US-09-962-360B-9

  Query Match             98.3%;  Score 169;  DB 10;  Length 42;
  Best Local Similarity   94.3%;  Pred. No. 6.6e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
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RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Botulinum
;  TITLE OF INVENTION:  Serotype A/E Toxins
;  FILE REFERENCE: P-AR 4803
;  CURRENT APPLICATION NUMBER: US/09/942,024
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;    LENGTH: 116
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-942-024-4

  Query Match             98.3%;  Score 169;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Botulinum
;  TITLE OF INVENTION:  Serotype A/E Toxins
;  FILE REFERENCE: P-AR 4803
;  CURRENT APPLICATION NUMBER: US/09/942,024
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;    LENGTH: 116
;    TYPE: PRT
;    ORGANISM: Mus musculus
US-09-942-024-17

  Query Match             98.3%;  Score 169;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Botulinum
;  TITLE OF INVENTION:  Serotype A/E Toxins
;  FILE REFERENCE: P-AR 4803
;  CURRENT APPLICATION NUMBER: US/09/942,024
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;    LENGTH: 116
;    TYPE: PRT
;    ORGANISM: Bos taurus
US-09-942-024-18

  Query Match             98.3%;  Score 169;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Clostridial
;  TITLE OF INVENTION:  Toxins
;  FILE REFERENCE: P-AR 4802
;  CURRENT APPLICATION NUMBER: US/09/942,098
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;    LENGTH: 116
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-942-098-4

  Query Match             98.3%;  Score 169;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Clostridial
;  TITLE OF INVENTION:  Toxins
;  FILE REFERENCE: P-AR 4802
;  CURRENT APPLICATION NUMBER: US/09/942,098
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;    LENGTH: 116
;    TYPE: PRT
;    ORGANISM: Mus musculus
US-09-942-098-17

  Query Match             98.3%;  Score 169;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 7
US-09-942-098-18
; Sequence 18, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Clostridial
;  TITLE OF INVENTION:  Toxins
;  FILE REFERENCE: P-AR 4802
;  CURRENT APPLICATION NUMBER: US/09/942,098
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-942-098-18

  Query Match             98.3%;  Score 169;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 8
US-10-357-028-10
; Sequence 10, Application US/10357028
; Publication No. US20030180931A1
;   GENERAL INFORMATION:
;        APPLICANT: Stuart, Susan G.
;                   Hawkins, Phillip R.
;                   Seilhamer, Jeffrey J.
;                   Murry, Lynn E.
;        TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
;        NUMBER OF SEQUENCES: 51
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Incyte Pharmaceuticals, Inc.
;             STREET: 3174 Porter Drive
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: U.S.
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 1.5
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/357,028
;             FILING DATE: 29-Jan-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/483,665
;             FILING DATE: Herewith
;             APPLICATION NUMBER: 08/621,018
;             FILING DATE: March 22, 1996
;             APPLICATION NUMBER: 08/409,373
;             FILING DATE: March 23, 1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hamlet-Cox, Diana
;             REGISTRATION NUMBER: 33,302
;             REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-855-0555
;             TELEFAX: 650-849-8886
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 116 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        IMMEDIATE SOURCE:
;             LIBRARY: GENBANK
;             CLONE: GI 433075
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-357-028-10

  Query Match             98.3%;  Score 169;  DB 14;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 9
US-10-261-161-11
; Sequence 11, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
;  APPLICANT: Fernandez-Salas, Ester
;  APPLICANT:  Steward, Lance E.
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
;  TITLE OF INVENTION:  Transfer (FRET) Assays For Clostridial Toxins
;  FILE REFERENCE: P-AR 4804
;  CURRENT APPLICATION NUMBER: US/10/261,161
;  CURRENT FILING DATE:  2002-09-27
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-261-161-11

  Query Match             98.3%;  Score 169;  DB 15;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 10
US-10-261-161-12
; Sequence 12, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
;  APPLICANT: Fernandez-Salas, Ester
;  APPLICANT:  Steward, Lance E.
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
;  TITLE OF INVENTION:  Transfer (FRET) Assays For Clostridial Toxins
;  FILE REFERENCE: P-AR 4804
;  CURRENT APPLICATION NUMBER: US/10/261,161
;  CURRENT FILING DATE:  2002-09-27
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 116
;   TYPE: PRT
```

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;  ORGANISM: Mus musculus
US-10-261-161-12

  Query Match             98.3%;  Score 169;  DB 15;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 11
US-10-261-161-13
; Sequence 13, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
;  APPLICANT: Fernandez-Salas, Ester
;  APPLICANT:  Steward, Lance E.
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
;  TITLE OF INVENTION:  Transfer (FRET) Assays For Clostridial Toxins
;  FILE REFERENCE: P-AR 4804
;  CURRENT APPLICATION NUMBER: US/10/261,161
;  CURRENT FILING DATE:  2002-09-27
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;  LENGTH: 116
;  TYPE: PRT
;  ORGANISM: Bos taurus
US-10-261-161-13

  Query Match             98.3%;  Score 169;  DB 15;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 12
US-09-293-670-55
; Sequence 55, Application US/09293670
; Publication No. US20030190684A1
; GENERAL INFORMATION:
;  APPLICANT: Fisher, Joseph
;  APPLICANT: Lorens, James
;  APPLICANT: Payan, Donald
;  APPLICANT: Rossi, Alexander
;  TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in
;  TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule
;  TITLE OF INVENTION: Libraries
;  FILE REFERENCE: A68104/DJB/RMS/DAV
;  CURRENT APPLICATION NUMBER: US/09/293,670
;  CURRENT FILING DATE: 1999-04-16
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
;  LENGTH: 607
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:  synthetic
US-09-293-670-55

  Query Match             98.3%;  Score 169;  DB 10;  Length 607;
  Best Local Similarity   94.3%;  Pred. No. 9.8e-15;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||
Db         61 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 95


RESULT 13
US-09-962-360B-3
; Sequence 3, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
;    /9
;  APPLICANT: Schmidt, James J.
;  APPLICANT:  Stafford, Robert G.
;  TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
;  TITLE OF INVENTION:  Neurotoxins
;  FILE REFERENCE: 003/224/SAP
;  CURRENT APPLICATION NUMBER: US/09/962,360B
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/235,050
;  PRIOR FILING DATE: 2001-09-25
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 3
;  LENGTH: 35
;  TYPE: PRT
;  ORGANISM: Artificial sequence
;  FEATURE:
;  OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: 14 and 20
;  OTHER INFORMATION: Xaa at 14 is N(epsilon)-2,4-(dinitrophenyl)-lysine and Xaa at 20 i
;  OTHER INFORMATION: (fluresceinyl)-cysteine
US-09-962-360B-3

  Query Match             97.7%;  Score 168;  DB 10;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||||||||||||||||||||||
Db          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35


RESULT 14
US-10-357-028-11
; Sequence 11, Application US/10357028
; Publication No. US20030180931A1
;  GENERAL INFORMATION:
;       APPLICANT: Stuart, Susan G.
;                  Hawkins, Phillip R.
;                  Seilhamer, Jeffrey J.
;                  Murry, Lynn E.
;       TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
;       NUMBER OF SEQUENCES: 51
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Incyte Pharmaceuticals, Inc.
;            STREET: 3174 Porter Drive
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: U.S.
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ Version 1.5
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/357,028
;            FILING DATE: 29-Jan-2003
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/483,665
;            FILING DATE: Herewith
;            APPLICATION NUMBER: 08/621,018
;            FILING DATE: March 22, 1996
```

; APPLICATION NUMBER: 08/409,373
; FILING DATE: March 23, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-Cox, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-849-8886
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 606978
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-357-028-11

Query Match 97.1%; Score 167; DB 14; Length 82;
Best Local Similarity 91.4%; Pred. No. 2.4e-15;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| |||||||||||||:|
Db 26 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 60

RESULT 15
US-09-942-024-19
; Sequence 19, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-942-024-19

Query Match 97.1%; Score 167; DB 10; Length 114;
Best Local Similarity 91.4%; Pred. No. 3.4e-15;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| |||||||||||||:|
Db 58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 92

Search completed: November 1, 2004, 18:23:47
Job time : 70.0625 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 ; Search time 18.125 Seconds
(without alignments)
185.798 Million cell updates/sec

Title: US-10-802-574-3
Perfect score: 172
Sequence: 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	169	98.3	116	2	B38315	synaptobrevin 2 -
2	169	98.3	116	2	JN0011	synaptobrevin 2 -
3	169	98.3	116	2	B34288	synaptobrevin 2 -
4	164	95.3	103	2	S35077	cellubrevin - rat
5	164	95.3	118	2	S52747	Vampl protein - hu
6	164	95.3	118	2	A38315	synaptobrevin 1 -
7	164	95.3	120	2	A32146	vesicle-associated
8	157	91.3	118	2	A34288	vesicle-associated
9	154	89.5	125	2	S40153	synaptobrevin - lo
10	152	88.4	109	2	T33239	synaptobrevin SNB-
11	115	66.9	32	2	S35555	vesicle-associated
12	115	66.9	32	2	S35554	vesicle-associated
13	115	66.9	32	2	S35552	vesicle-associated
14	112	65.1	132	2	JC1522	synaptobrevin isof
15	112	65.1	152	2	JC1521	synaptobrevin isof
16	108	62.8	32	2	S35553	vesicle-associated
17	106	61.6	145	2	T21318	hypothetical prote
18	87	50.6	223	2	S47654	integral membrane
19	81	47.1	115	2	S62059	synaptobrevin homo
20	75	43.6	121	2	T39073	synaptobrevin homo
21	71	41.3	117	2	S31250	synaptobrevin homo
22	68	39.5	220	2	T00801	probable synaptobr
23	64	37.2	60	2	D44088	homeotic protein H
24	64	37.2	221	2	F84741	probable synaptobr
25	63	36.6	1237	1	GNFF42	HIV-1 retropepsin
26	62	36.0	175	2	D86180	hypothetical prote
27	59	34.3	251	2	S64927	probable membrane
28	58	33.7	210	2	T16595	hypothetical prote
29	57.5	33.4	229	2	F86180	hypothetical prote
30	57	33.1	240	2	T47589	synaptobrevin-like
31	55	32.0	219	2	T04630	synaptobrevin homo
32	54	31.4	102	2	S44781	C30A5.4 protein -
33	54	31.4	102	2	T24909	hypothetical prote
34	54	31.4	302	2	S69725	hypothetical prote
35	53	30.8	499	2	T18791	gamma-aminobutyric
36	53	30.8	855	2	T29775	hypothetical prote
37	52.5	30.5	2326	2	T29140	hypothetical prote
38	52	30.2	183	1	TLBP84	tail fiber assembl
39	52	30.2	183	2	S13240	tail fiber assembl
40	52	30.2	788	2	T44262	transducer protein
41	52	30.2	789	2	E84236	Htr6 transducer [i
42	52	30.2	1116	2	T42213	m-tomosyn, isoform
43	51.5	29.9	1278	2	T27925	hypothetical prote
44	51	29.7	609	2	AB0500	glutamine-fructose
45	51	29.7	1281	2	JC5368	dynactin 1 - mouse

ALIGNMENTS

RESULT 1
B38315
synaptobrevin 2 - human
C;Species: Homo sapiens (man)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C;Accession: B38315
R;Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A;Title: Structures and chromosomal localizations of two human genes encoding synaptobrev
A;Reference number: A38315; MUID:91009161; PMID:1976629
A;Accession: B38315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-116 <ARC>
A;Cross-references: UNIPROT:P19065; GB:M36205; GB:J05611; NID:g338630; PIDN:AAA60604.1; P
C;Genetics:
A;Gene: GDB:SYB2; VAMP-2
A;Cross-references: GDB:125293; OMIM:185881
A;Map position: 17pter-17p12
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

Query Match 98.3%; Score 169; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94
```

RESULT 2
JN0011
synaptobrevin 2 - bovine
N;Alternate names: SNAP receptor
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: JN0011; S36811; S32363
R;Suedhof, T.C.; Baumert, M.; Perin, M.S.; Jahn, R.
Neuron 2, 1475-1481, 1989
A;Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.
A;Reference number: A93413; MUID:90180466; PMID:2560644
A;Accession: JN0011
A;Molecule type: mRNA
A;Residues: 1-116 <SUE>
A;Cross-references: UNIPROT:P19065; GB:X76199; NID:g433075; PIDN:CAA53792.1; PID:g433076
A;Experimental source: brain
R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyna
A;Reference number: S36811; MUID:93374072; PMID:8365494
A;Accession: S36811

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A;Molecule type: mRNA
A;Residues: 'X',48-79 <HOR>
A;Experimental source: brain
R;Soellner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Geromanos, S.; Tem
Nature 362, 318-324, 1993
A;Title: SNAP receptors implicated in vesicle targeting and fusion.
A;Reference number: S32360; MUID:93205116; PMID:8455717
A;Accession: S32363
A;Molecule type: protein
A;Residues: 31-47,'X',49-55,'X',57-59;67-82 <SOE>
A;Experimental source: brain
C;Comment: This protein is an intrinsic membrane protein of small synaptic vesicles.
C;Superfamily: synaptobrevin
C;Keywords: acetylated amino end; membrane trafficking; transmembrane protein
F;2-116/Product: synaptobrevin 2 #status predicted <MAT>
F;95-114/Domain: transmembrane #status predicted <TMM>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

  Query Match             98.3%;  Score 169;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||| ||||| ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 3
B34288
synaptobrevin 2 - rat
N;Alternate names: vesicle-associated membrane protein 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
C;Accession: B34288; S27125
R;Elferink, L.A.; Trimble, W.S.; Scheller, R.H.
J. Biol. Chem. 264, 11061-11064, 1989
A;Title: Two vesicle-associated membrane protein genes are differentially expressed in t
A;Reference number: A34288; MUID:89291844; PMID:2472388
A;Accession: B34288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <ELF>
A;Cross-references: UNIPROT:Q64357; GB:M24105; GB:J04827; NID:g207626; PIDN:AAA42321.1;
R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R
Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt
A;Reference number: S27125; MUID:93063293; PMID:1331807
A;Accession: S27125
A;Molecule type: protein
A;Residues: 77-99,'X',101 <SCH>
C;Superfamily: synaptobrevin
C;Keywords: membrane protein; membrane trafficking; synaptic vesicle

  Query Match             98.3%;  Score 169;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||| ||||| ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 4
S35077
cellubrevin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S35077
R;McMahon, H.T.; Ushkaryov, Y.A.; Edelmann, L.; Link, E.; Binz, T.; Niemann, H.; Jahn, R
Nature 364, 346-349, 1993
A;Title: Cellubrevin is a ubiquitous tetanus-toxin substrate homologous to a putative sy
A;Reference number: S35077; MUID:93323976; PMID:8332193
A;Accession: S35077
A;Molecule type: mRNA
A;Residues: 1-103 <MCM>
A;Cross-references: UNIPROT:Q64271; GB:S63830; NID:g388482; PIDN:AAB27554.1; PID:g388483
C;Superfamily: synaptobrevin

  Query Match             95.3%;  Score 164;  DB 2;  Length 103;
  Best Local Similarity   91.4%;  Pred. No. 1.3e-15;
  Matches   32;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||| ||||| ||||||||||||| |
Db         47 LSELDDRADALQAGASQFETSAAKLKRKYWWKNCK 81


RESULT 5
S52747
Vamp1 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52747
R;Gough, K.H.; Verkuylen, A.; Cosgrove, L.; Frenkel, M.J.; Ward, C.W.
submitted to the EMBL Data Library, December 1994
A;Description: Isolation and sequence analysis of SNAREs from human skeletal muscle.
A;Reference number: S52747
A;Accession: S52747
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <GOU>
A;Cross-references: UNIPROT:P23763; EMBL:Z48924; NID:g758107; PIDN:CAA88760.1; PID:g7581(
C;Superfamily: synaptobrevin

  Query Match             95.3%;  Score 164;  DB 2;  Length 118;
  Best Local Similarity   91.4%;  Pred. No. 1.5e-15;
  Matches   32;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||| ||||| ||||||||||||| |
Db         62 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 96


RESULT 6
A38315
synaptobrevin 1 - human
C;Species: Homo sapiens (man)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C;Accession: A38315
R;Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A;Title: Structures and chromosomal localizations of two human genes encoding synaptobrev
A;Reference number: A38315; MUID:91009161; PMID:1976629
A;Accession: A38315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <ARC>
A;Cross-references: UNIPROT:P23763; GB:M36200; GB:J05611; NID:g338623; PIDN:AAA60603.1; P
C;Genetics:
A;Gene: GDB:SYB1; VAMP-1
A;Cross-references: GDB:125292; OMIM:185880
A;Map position: 12p-12p
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

  Query Match             95.3%;  Score 164;  DB 2;  Length 118;
  Best Local Similarity   91.4%;  Pred. No. 1.5e-15;
  Matches   32;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||| ||||| ||||||||||||| |
Db         62 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 96


RESULT 7
A32146
```

vesicle-associated membrane protein 1 - Pacific electric ray
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C;Accession: A32146
R;Trimble, W.S.; Cowan, D.M.; Scheller, R.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 4538-4542, 1988
A;Title: VAMP-1: a synaptic vesicle-associated integral membrane protein.
A;Reference number: A32146; MUID:88248054; PMID:3380805
A;Accession: A32146
A;Molecule type: mRNA
A;Residues: 1-120 <TRI>
A;Cross-references: UNIPROT:P13701; EMBL:J03777; NID:g213245; PIDN:AAA49286.1; PID:g2132
C;Superfamily: synaptobrevin
C;Keywords: membrane protein

Query Match 95.3%; Score 164; DB 2; Length 120;
Best Local Similarity 91.4%; Pred. No. 1.5e-15;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| ||||| |||||||||||||
Db 64 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 98

RESULT 8
A34288
vesicle-associated membrane protein 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34288
R;Elferink, L.A.; Trimble, W.S.; Scheller, R.H.
J. Biol. Chem. 264, 11061-11064, 1989
A;Title: Two vesicle-associated membrane protein genes are differentially expressed in t
A;Reference number: A34288; MUID:89291844; PMID:2472388
A;Accession: A34288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <ELF>
A;Cross-references: UNIPROT:Q63666; GB:M24104; GB:J04827; NID:g207628; PIDN:AAA42322.1;
C;Superfamily: synaptobrevin
C;Keywords: membrane protein

Query Match 91.3%; Score 157; DB 2; Length 118;
Best Local Similarity 88.6%; Pred. No. 1.4e-14;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||||||||||||| || || |||||||||||||
Db 62 LSELDDRADALQAGASVFESSAAKLKRKYWWKNCK 96

RESULT 9
S40153
synaptobrevin - longfin squid
C;Species: Loligo pealeii (longfin squid)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40153
R;Bommert, K.; Kistner, A.; Hasermann, E.; Betz, H.
submitted to the EMBL Data Library, August 1993
A;Description: Conservation of primary structure and clostridial neurotoxin cleavage sit
A;Reference number: S40153
A;Accession: S40153
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <BOM>
A;Cross-references: UNIPROT:P47194; EMBL:X74748; NID:g437855; PIDN:CAA52766.1; PID:g4378
C;Superfamily: synaptobrevin

Query Match 89.5%; Score 154; DB 2; Length 125;
Best Local Similarity 82.9%; Pred. No. 3.8e-14;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
:|||||||||||| ||||| || |||||:|||| |
Db 69 ISELDDRADALQAGASQFEASAGKLKRKFWWKNCK 103

RESULT 10
T33239
synaptobrevin SNB-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33239
R;Greco, T.; Bradshaw, H.; O'Brien, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T10H9.
A;Reference number: Z21306
A;Accession: T33239
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-109 <GRE>
A;Cross-references: UNIPROT:O02495; EMBL:AF067949; PIDN:AAC19234.1; GSPDB:GN00023; CESP:T
A;Experimental source: strain Bristol N2; clone T10H9
C;Genetics:
A;Gene: SNB-1; CESP:T10H9.4
A;Map position: 5
A;Introns: 39/3
C;Superfamily: synaptobrevin

Query Match 88.4%; Score 152; DB 2; Length 109;
Best Local Similarity 82.9%; Pred. No. 6.3e-14;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
||:|||||||| ||||| ||| |||||||||:|
Db 52 LSQLDDRADALQEGASQFEKSAATLKRKYWWKNIK 86

RESULT 11
S35555
vesicle-associated membrane protein 2 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S35555
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35555
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q7LZ64
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

Query Match 66.9%; Score 115; DB 2; Length 32;
Best Local Similarity 92.6%; Pred. No. 2.4e-09;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFEXSAAKLKR 27
||||||||||||| ||||| |||||||
Db 6 LSELDDRADALQAGASQFETSAAKLKR 32

RESULT 12
S35554
vesicle-associated membrane protein 2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S35554
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35554
A;Status: preliminary

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A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:O35619
C;Superfamily: synaptobrevin

  Query Match             66.9%;  Score 115;  DB 2;  Length 32;
  Best Local Similarity   92.6%;  Pred. No. 2.4e-09;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKR 27
              |||||||||||||| ||||| |||||||
Db          6 LSELDDRADALQAGASQFETSAAKLKR 32


RESULT 13
S35552
vesicle-associated membrane protein 1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S35552
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35552
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q9CXX2
C;Superfamily: synaptobrevin

  Query Match             66.9%;  Score 115;  DB 2;  Length 32;
  Best Local Similarity   92.6%;  Pred. No. 2.4e-09;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKR 27
              |||||||||||||| ||||| |||||||
Db          6 LSELDDRADALQAGASQFESSAAKLKR 32


RESULT 14
JC1522
synaptobrevin isoform B - fruit fly (Drosophila melanogaster)
N;Alternate names: vesicle-associated membrane protein B
C;Species: Drosophila melanogaster
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: JC1522
R;Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.
Gene 131, 175-181, 1993
A;Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene
A;Reference number: JC1521; MUID:94010306; PMID:8406010
A;Accession: JC1522
A;Molecule type: DNA
A;Residues: 1-132 <CHI>
A;Cross-references: UNIPROT:P18489; GB:L14270; NID:g290281; PIDN:AAA28923.1; PID:g290282
A;Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue
C;Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobre
C;Genetics:
A;Gene: syb
A;Cross-references: FlyBase:FBgn0003660
A;Introns: 16/2; 128/1
C;Superfamily: synaptobrevin
C;Keywords: membrane protein; synaptic vesicle

  Query Match             65.1%;  Score 112;  DB 2;  Length 132;
  Best Local Similarity   62.9%;  Pred. No. 2.6e-08;
  Matches   22;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              |||| :||| |:  ||| |  | ||||| || |:|
Db         76 LSELGERADQLEQGASQSEQQAGKLKRKQWWANMK 110


RESULT 15
JC1521
synaptobrevin isoform A - fruit fly (Drosophila melanogaster)
N;Alternate names: vesicle-associated membrane protein A
C;Species: Drosophila melanogaster
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: JC1521; JN0012
R;Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.
Gene 131, 175-181, 1993
A;Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene
A;Reference number: JC1521; MUID:94010306; PMID:8406010
A;Accession: JC1521
A;Molecule type: DNA
A;Residues: 1-152 <CHI>
A;Cross-references: UNIPROT:P18489; GB:L14270; NID:g290281; PIDN:AAA28924.1; PID:g290283
A;Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue
R;Suedhof, T.C.; Baumert, M.; Perin, M.S.; Jahn, R.
Neuron 2, 1475-1481, 1989
A;Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.
A;Reference number: A93413; MUID:90180466; PMID:2560644
A;Accession: JN0012
A;Molecule type: mRNA
A;Residues: 1-92,'F',94-152 <SUE>
C;Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobrev
C;Genetics:
A;Gene: syb
A;Cross-references: FlyBase:FBgn0003660
A;Introns: 16/2; 128/1
C;Superfamily: synaptobrevin
C;Keywords: synaptic vesicle; transmembrane protein
F;111-130/Domain: transmembrane #status predicted <TMM>

  Query Match             65.1%;  Score 112;  DB 2;  Length 152;
  Best Local Similarity   62.9%;  Pred. No. 3e-08;
  Matches   22;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              |||| :||| |:  ||| |  | ||||| || |:|
Db         76 LSELGERADQLEQGASQSEQQAGKLKRKQWWANMK 110


Search completed: November  1, 2004, 17:53:51
Job time : 19.125 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 97.1875 Seconds
(without alignments)
207.209 Million cell updates/sec

Title: US-10-802-574-3
Perfect score: 172
Sequence: 1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	169	98.3	81	2	Q8HZX7	Q8hzx7 oryctolagus
2	169	98.3	114	2	Q6P835	Q6p835 xenopus tro
3	169	98.3	114	2	AAH61396	Aah61396 xenopus t
4	169	98.3	115	1	VAM2_HUMAN	P19065 homo sapien
5	169	98.3	115	1	VAM2_MOUSE	Q64357 mus musculu
6	169	98.3	116	2	Q9BUC2	Q9buc2 homo sapien
7	169	98.3	116	2	Q9N0Y0	Q9n0y0 macaca mula
8	169	98.3	116	2	O35619	O35619 mus musculu
9	169	98.3	116	2	AAH02737	Aah02737 homo sapi
10	169	98.3	116	2	AAH55105	Aah55105 mus muscu
11	169	98.3	116	2	BAC41125	Bac41125 mus muscu
12	169	98.3	135	2	Q9WUW2	Q9wuw2 rattus norv
13	169	98.3	142	2	Q8CHR4	Q8chr4 mus musculu
14	167	97.1	113	1	VAM2_XENLA	P47193 xenopus lae
15	167	97.1	114	2	AAH60344	Aah60344 xenopus l
16	164	95.3	99	1	VAM3_HUMAN	Q15836 homo sapien
17	164	95.3	103	1	VAM3_MOUSE	Q64271 mus musculu
18	164	95.3	103	2	AAG42468	Aag42468 mus muscu
19	164	95.3	103	2	AAH60045	Aah60045 mus muscu
20	164	95.3	103	2	BAC34586	Bac34586 mus muscu
21	164	95.3	103	2	BAC34723	Bac34723 mus muscu
22	164	95.3	117	2	Q8IVC9	Q8ivc9 homo sapien
23	164	95.3	117	2	Q6PFF3	Q6pff3 mus musculu
24	164	95.3	117	2	AAH57587	Aah57587 mus muscu
25	164	95.3	118	1	VAM1_HUMAN	P23763 homo sapien
26	164	95.3	118	1	VAM1_MOUSE	Q62442 mus musculu
27	164	95.3	118	2	BAC37151	Bac37151 mus muscu
28	164	95.3	120	1	SYB_TORCA	P13701 torpedo cal
29	164	95.3	182	2	Q9CXX2	Q9cxx2 mus musculu
30	163	94.8	114	2	O57345	O57345 xenopus lae
31	162	94.2	102	2	Q6IQK3	Q6iqk3 brachydanio
32	162	94.2	102	2	AAH71402	Aah71402 brachydan
33	162	94.2	119	2	Q6PBJ3	Q6pbj3 brachydanio
34	162	94.2	119	2	AAH59687	Aah59687 brachydan
35	160	93.0	100	2	Q9BRV4	Q9brv4 homo sapien
36	159	92.4	110	2	Q7SZZ5	Q7szz5 brachydanio
37	159	92.4	110	2	AAH59626	Aah59626 brachydan
38	159	92.4	112	2	O57432	O57432 fugu rubrip
39	157	91.3	116	2	Q8CH14	Q8ch14 rattus norv
40	157	91.3	117	2	O09025	O09025 rattus norv
41	157	91.3	118	1	VAM1_RAT	Q63666 rattus norv
42	155	90.1	86	2	Q6DLT0	Q6dlt0 lateolabrax
43	155	90.1	110	2	Q8T897	Q8t897 halocynthia
44	155	90.1	160	2	Q86FE0	Q86fe0 schistosoma
45	154	89.5	118	2	Q6DGI1	Q6dgi1 brachydanio

ALIGNMENTS

RESULT 1
Q8HZX7
ID Q8HZX7 PRELIMINARY; PRT; 81 AA.
AC Q8HZX7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptobrevin-2 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal collecting duct;
RX PubMed=12186952;
RA Gouraud S., Laera A., Calamita G., Carmosino M., Procino G.,
RA Rossetto O., Mannucci R., Rosenthal W., Svelto M., Valenti G.;
RT "Functional involvement of VAMP/synaptobrevin-2 in cAMP-stimulated
RT aquaporin 2 translocation in renal collecting duct cells.";
RL J. Cell Sci. 115:3667-3674(2002).
DR EMBL; AF262953; AAN14408.1; -.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin; 1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; Synaptobrevin; 1.
DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR PROSITE; PS50892; V_SNARE; 1.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9357 MW; 6F171CA14775860C CRC64;

Query Match 98.3%; Score 169; DB 2; Length 81;
Best Local Similarity 94.3%; Pred. No. 5.1e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         32 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 66
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RESULT 2
Q6P835
ID Q6P835 PRELIMINARY; PRT; 114 AA.
AC Q6P835;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75977.
GN Name=MGC75977;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.

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OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061396; AAH61396.1; -.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   114 AA;  12440 MW;  0EE3EADBDF2A1ABE CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 114;
  Best Local Similarity   94.3%;  Pred. No. 7.2e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              |||||||||||||| ||||| ||||||||||||||||
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 92


RESULT 3
AAH61396
ID   AAH61396    PRELIMINARY;      PRT;   114 AA.
AC   AAH61396;
DT   25-MAR-2004 (TrEMBLrel. 27, Created)
DT   25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC75977.
GN   MGC75977.
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061396; AAH61396.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   114 AA;  12440 MW;  0EE3EADBDF2A1ABE CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 114;
  Best Local Similarity   94.3%;  Pred. No. 7.2e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              |||||||||||||| ||||| ||||||||||||||||
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 92


RESULT 4
VAM2_HUMAN
ID   VAM2_HUMAN     STANDARD;      PRT;   115 AA.
AC   P19065;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).
GN   Name=VAMP2; Synonyms=SYB2;
OS   Homo sapiens (Human), and
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606, 9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human;
RX   MEDLINE=91009161; PubMed=1976629;
RA   Archer B.T. III, Oezcelik T., Jahn R., Francke U., Suedhof T.C.;
RT   "Structures and chromosomal localizations of two human genes encoding
RT   synaptobrevins 1 and 2.";
RL   J. Biol. Chem. 265:17267-17273(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human; TISSUE=Peripheral blood;
RA   Nabokina S.M., Lazo P.A., Mollinedo F.;
RT   "Expression of VAMP genes in human neutrophils.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human; TISSUE=Blood;
RA   Taruscio D., Zoraqi K.G., Falbo V.;
RT   "Genomic structure of human SYB2 gene.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Bovine;
RX   MEDLINE=90180466; PubMed=2560644;
RA   Suedhof T.C., Baumert M., Perin M.S., Jahn R.;
RT   "A synaptic vesicle membrane protein is conserved from mammals to
RT   Drosophila.";
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RL   Neuron 2:1475-1481(1989).
RN   [5]
RP   SEQUENCE OF 31-59 AND 67-82, AND ACETYLATION.
RC   SPECIES=Bovine;
RX   MEDLINE=93205116; PubMed=8455717;
RA   Soellner T., Whiteheart S.W., Brunner M., Erdjument-Bromage H.,
RA   Geromanos S., Tempst P., Rothman J.E.;
RT   "SNAP receptors implicated in vesicle targeting and fusion.";
RL   Nature 362:318-324(1993).
RN   [6]
RP   TISSUE SPECIFICITY.
RC   SPECIES=Human;
RX   MEDLINE=96332494; PubMed=8760387;
RA   Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
RA   Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
RA   Ward C.W.;
RT   "Insulin-responsive tissues contain the core complex protein SNAP-25
RT   (synaptosomal-associated protein 25) A and B isoforms in addition to
RT   syntaxin 4 and synaptobrevins 1 and 2.";
RL   Biochem. J. 317:945-954(1996).
RN   [7]
RP   TOPOLOGY.
RC   SPECIES=Human;
RX   MEDLINE=95137000; PubMed=7835332;
RA   Kutay U., Ahnert-Hilger G., Hartmann E., Wiedenmann B., Rapoport T.A.;
RT   "Transport route for synaptobrevin via a novel pathway of insertion
RT   into the endoplasmic reticulum membrane.";
RL   EMBO J. 14:217-223(1995).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-88 IN COMPLEX WITH BOTB.
RC   SPECIES=Human;
RX   MEDLINE=20392548; PubMed=10932255; DOI=10.1038/77997;
RA   Hanson M.A., Stevens R.C.;
RT   "Cocrystal structure of synaptobrevin-II bound to botulinum neurotoxin
RT   type B at 2.0 A resolution.";
RL   Nat. Struct. Biol. 7:687-692(2000).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBUNIT: Interacts with VAPA and VAPB.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- TISSUE SPECIFICITY: Nervous system and skeletal muscle.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M36205; AAA60604.1; -.
DR   EMBL; M36201; AAA60604.1; JOINED.
DR   EMBL; M36202; AAA60604.1; JOINED.
DR   EMBL; M36203; AAA60604.1; JOINED.
DR   EMBL; M36204; AAA60604.1; JOINED.
DR   EMBL; AJ225044; CAA12385.1; -.
DR   EMBL; AF135372; AAF15551.1; -.
DR   EMBL; X76199; CAA53792.1; -.
DR   PIR; B38315; B38315.
DR   PIR; JN0011; JN0011.
DR   PDB; 1F83; X-ray; B=52-75, C=76-87.
DR   Genew; HGNC:12643; VAMP2.
DR   MIM; 185881; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   3D-structure; Acetylation; Coiled coil; Direct protein sequencing;
KW   Multigene family; Synapse; Synaptosome; Transmembrane.
FT   INIT_MET      0      0
FT   DOMAIN        1     93       Cytoplasmic (Potential).
FT   TRANSMEM     94    113       Anchor for type IV membrane protein
FT                                 (Potential).
FT   DOMAIN      114    115       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine.
FT   DOMAIN       30     90       v-SNARE coiled-coil homology.
SQ   SEQUENCE   115 AA;  12517 MW;  388B79F0D21AD81E CRC64;

  Query Match             98.3%;  Score 169;  DB 1;  Length 115;
  Best Local Similarity   94.3%;  Pred. No. 7.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93


RESULT 5
VAM2_MOUSE
ID   VAM2_MOUSE     STANDARD;      PRT;   115 AA.
AC   Q64357;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).
GN   Name=Vamp2; Synonyms=Syb2;
OS   Mus musculus (Mouse), and
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090, 10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=89291844; PubMed=2472388;
RA   Elferink L.A., Trimble W.S., Scheller R.H.;
RT   "Two vesicle-associated membrane protein genes are differentially
RT   expressed in the rat central nervous system.";
RL   J. Biol. Chem. 264:11061-11064(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Mouse;
RX   MEDLINE=98104125; PubMed=9430681;
RA   Martin L.B., Shewan A., Millar C.A., Gould G.W., James D.E.;
RT   "Vesicle-associated membrane protein 2 plays a specific role in the
RT   insulin-dependent trafficking of the facilitative glucose transporter
RT   GLUT4 in 3T3-L1 adipocytes.";
RL   J. Biol. Chem. 273:1444-1452(1998).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-96 IN COMPLEX WITH STX1A
RP   AND SNAP25.
RC   SPECIES=Rat;
RX   MEDLINE=98430524; PubMed=9759724; DOI=10.1038/26412;
RA   Sutton R.B., Fasshauer D., Jahn R., Brunger A.T.;
RT   "Crystal structure of a SNARE complex involved in synaptic exocytosis
RT   at 2.4 A resolution.";
RL   Nature 395:347-353(1998).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 29-93 IN COMPLEX WITH STX1A;
RP   CPLX1 AND SNAP25, AND NMR ANALYSIS.
RC   SPECIES=Rat;
RX   MEDLINE=21822661; PubMed=11832227;
RA   Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
RA   Suedhof T.C., Rizo J.;
RT   "Three-dimensional structure of the complexin/SNARE complex.";
RL   Neuron 33:397-409(2002).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 28-89 IN COMPLEX WITH STX1A
RP   AND SNAP25.
RC   SPECIES=Rat;
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RX   MEDLINE=22499607; PubMed=12496247; DOI=10.1074/jbc.M211889200;
RA   Ernst J.A., Brunger A.T.;
RT   "High resolution structure, stability, and synaptotagmin binding of a
RT   truncated neuronal SNARE complex.";
RL   J. Biol. Chem. 278:8630-8636(2003).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBUNIT: Interacts with VAPA and VAPB (By similarity). Part of the
CC       SNARE core complex containing SNAP25, VAMP2 and STX1A. This
CC       complex binds to CPLX1.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- TISSUE SPECIFICITY: Nervous system specific. A higher level
CC       expression is seen in the brain as compared to the spinal cord.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M24105; AAA42321.1; -.
DR   EMBL; U60150; AAB03463.1; -.
DR   PIR; B34288; B34288.
DR   PDB; 1KIL; X-ray; A=26-91.
DR   PDB; 1N7S; X-ray; A=26-88.
DR   PDB; 1SFC; X-ray; A/E/I=1-95.
DR   MGD; MGI:1313277; Vamp2.
DR   RGD; 3949; Vamp2.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   3D-structure; Acetylation; Coiled coil; Multigene family;
KW   Polymorphism; Synapse; Synaptosome; Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     93       Cytoplasmic (Potential).
FT   TRANSMEM     94    113       Anchor for type IV membrane protein
FT                                (Potential).
FT   DOMAIN      114    115       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine (By similarity).
FT   DOMAIN       30     90       v-SNARE coiled-coil homology.
FT   VARIANT     110    110       I -> II.
FT   VARIANT     111    111       V -> I.
FT   HELIX        28     87
SQ   SEQUENCE   115 AA;  12559 MW;  EA400D6291ABF0BC CRC64;

  Query Match             98.3%;  Score 169;  DB 1;  Length 115;
  Best Local Similarity   94.3%;  Pred. No. 7.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93


RESULT 6
Q9BUC2
ID   Q9BUC2      PRELIMINARY;      PRT;   116 AA.
AC   Q9BUC2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Vesicle-associated membrane protein 2 (Synaptobrevin 2).
GN   Name=VAMP2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, Lung, and Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002737; AAH02737.3; -.
DR   EMBL; BC019608; AAH19608.1; -.
DR   EMBL; BC033870; AAH33870.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 7
Q9N0Y0
ID   Q9N0Y0      PRELIMINARY;      PRT;   116 AA.
AC   Q9N0Y0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   VAMP-2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hippocampus;
RA   Jensen M.J., Smith L.A.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF240769; AAF64476.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 8
O35619
ID   O35619      PRELIMINARY;      PRT;   116 AA.
AC   O35619;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vesicle associated membrane protein 2.
GN   Name=Vamp2; Synonyms=mVAMP-2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Olken S.K., Doerre S., Corley R.B.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF007168; AAB62931.1; -.
DR   PIR; S35554; S35554.
DR   HSSP; Q9WUW2; 1SFC.
DR   MGD; MGI:1313277; Vamp2.
DR   GO; GO:0030141; C:secretory granule; IDA.
DR   GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR   GO; GO:0042589; C:zymogen granule membrane; IDA.
DR   GO; GO:0005516; F:calmodulin binding; IDA.
DR   GO; GO:0005543; F:phospholipid binding; IDA.
DR   GO; GO:0000149; F:SNARE binding; IDA.
DR   GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.
DR   GO; GO:0017157; P:regulation of exocytosis; IDA.
DR   GO; GO:0016083; P:synaptic vesicle fusion; IMP.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12677 MW;  4E1D0D56B5409D0A CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 9
AAH02737
ID   AAH02737    PRELIMINARY;      PRT;   116 AA.
AC   AAH02737;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Vesicle-associated membrane protein 2 (Synaptobrevin 2).
GN   VAMP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002737; AAH02737.3; -.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 10
AAH55105
ID   AAH55105    PRELIMINARY;      PRT;   116 AA.
AC   AAH55105;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Vesicle-associated membrane protein 2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055105; AAH55105.1; -.
SQ   SEQUENCE   116 AA;  12691 MW;  4A0D0D56B5409D0A CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 11
BAC41125
ID   BAC41125    PRELIMINARY;      PRT;   116 AA.
AC   BAC41125;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   15 days embryo brain cDNA, RIKEN full-length enriched library,
DE   clone:G630012G02 product:unclassifiable, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK090178; BAC41125.1; -.
SQ   SEQUENCE   116 AA;  12691 MW;  4A0D0D56B5409D0A CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.3e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 12
Q9WUW2
ID   Q9WUW2      PRELIMINARY;      PRT;   135 AA.
AC   Q9WUW2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vesicle associated membrane protein 2B.
GN   Name=vamp2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=99297576; PubMed=10371166;
RA   Mandic R., Lowe A.W.;
RT   "Characterization of an alternatively spliced isoform of rat vesicle
RT   associated membrane protein-2 (VAMP-2).";
RL   FEBS Lett. 451:209-213(1999).
DR   EMBL; AJ133104; CAB43509.1; -.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
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DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   135 AA;  14509 MW;  F37D14A87BDAB1F6 CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 135;
  Best Local Similarity   94.3%;  Pred. No. 8.6e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 13
Q8CHR4
ID   Q8CHR4      PRELIMINARY;      PRT;   142 AA.
AC   Q8CHR4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vamp2 protein (Fragment).
GN   Name=Vamp2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA   Strausberg R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC039745; AAH39745.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   MGD; MGI:1313277; Vamp2.
DR   GO; GO:0030141; C:secretory granule; IDA.
DR   GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR   GO; GO:0042589; C:zymogen granule membrane; IDA.
DR   GO; GO:0005516; F:calmodulin binding; IDA.
DR   GO; GO:0005543; F:phospholipid binding; IDA.
DR   GO; GO:0000149; F:SNARE binding; IDA.
DR   GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.
DR   GO; GO:0017157; P:regulation of exocytosis; IDA.
DR   GO; GO:0016083; P:synaptic vesicle fusion; IMP.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   142 AA;  15313 MW;  F1B0C9C9B495B776 CRC64;

  Query Match             98.3%;  Score 169;  DB 2;  Length 142;
  Best Local Similarity   94.3%;  Pred. No. 9.1e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| ||||||||||||||||
Db         86 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 120


RESULT 14
VAM2_XENLA
ID   VAM2_XENLA     STANDARD;      PRT;   113 AA.
AC   P47193;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2)
DE   (SYBII).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang X.-H., Poo M.-M.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 32-113 FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=95324415; PubMed=7601005;
RA   Knecht A.K., Good P.J., Dawid I.B., Harland R.M.;
RT   "Dorsal-ventral patterning and differentiation of noggin-induced
RT   neural tissue in the absence of mesoderm.";
RL   Development 121:1927-1935(1995).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF035017; AAB88138.1; -.
DR   EMBL; U16801; AAA81376.1; -.
DR   HSSP; P19065; 1F83.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Acetylation; Coiled coil; Multigene family; Synapse; Synaptosome;
KW   Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     91       Cytoplasmic (Potential).
FT   TRANSMEM     92    110       Anchor for type IV membrane protein
FT                                (Potential).
FT   DOMAIN      111    113       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine (By similarity).
FT   DOMAIN       28     88       v-SNARE coiled-coil homology.
SQ   SEQUENCE   113 AA;  12341 MW;  6EC6C937B29BC6AB CRC64;
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Query Match 97.1%; Score 167; DB 1; Length 113;
Best Local Similarity 91.4%; Pred. No. 1.4e-15;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
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Db         57 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 91
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RESULT 15
AAH60344
ID AAH60344 PRELIMINARY; PRT; 114 AA.
AC AAH60344;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Vamp2-B-prov protein.
GN VAMP2-B-PROV.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC060344; AAH60344.1; -.
SQ SEQUENCE 114 AA; 12472 MW; AEF2EDDCDF2D1DBF CRC64;

Query Match 97.1%; Score 167; DB 2; Length 114;
Best Local Similarity 91.4%; Pred. No. 1.4e-15;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAXASQFEXSAAKLKRKYWWKNLK 35
              ||||||||||||| ||||| |||||||||||||:|
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 92
```

Search completed: November 1, 2004, 17:59:09
Job time : 99.1875 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 90 Seconds
(without alignments)
139.506 Million cell updates/sec

Title: US-10-802-574-4
Perfect score: 173
Sequence: 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	98.3	37	2	AAR86822	Aar86822 VAMP isof
2	170	98.3	40	4	AAB50301	Aab50301 VAMP2 pep
3	170	98.3	40	4	AAB48582	Aab48582 VAMP2 pep
4	170	98.3	42	5	AAO15163	Aao15163 Clostridi
5	170	98.3	54	3	AAB39482	Aab39482 Gene 49 h
6	170	98.3	62	2	AAR86821	Aar86821 VAMP isof
7	170	98.3	115	7	ADE57598	Ade57598 Human Pro
8	170	98.3	115	7	ADE57612	Ade57612 Rat Prote
9	170	98.3	115	7	ADE60831	Ade60831 Human Pro
10	170	98.3	115	7	ADE57606	Ade57606 Human Pro
11	170	98.3	115	7	ADE60829	Ade60829 Rat Prote
12	170	98.3	115	7	ADE57600	Ade57600 Rat Prote
13	170	98.3	115	7	ADE57604	Ade57604 Rat Prote
14	170	98.3	115	7	ADE57596	Ade57596 Rat Prote
15	170	98.3	115	7	ADE57602	Ade57602 Human Pro
16	170	98.3	115	7	ADE57610	Ade57610 Human Pro
17	170	98.3	115	7	ADE57592	Ade57592 Rat Prote
18	170	98.3	115	7	ADE57594	Ade57594 Human Pro
19	170	98.3	115	7	ADE57614	Ade57614 Human Pro
20	170	98.3	115	7	ADE57608	Ade57608 Rat Prote
21	170	98.3	116	2	AAW30104	Aaw30104 Vesicle-a
22	170	98.3	116	2	AAW43425	Aaw43425 Rat vesic
23	170	98.3	116	3	AAY88243	Aay88243 Bovine sy
24	170	98.3	116	5	ABP43681	Abp43681 VAMP-2 se
25	170	98.3	116	6	ABP76220	Abp76220 Human GEN
26	170	98.3	116	6	AAE36664	Aae36664 Human VAM
27	170	98.3	116	7	ABW01719	Abw01719 Bovine VA
28	170	98.3	116	7	ABW01718	Abw01718 Mouse VAM
29	170	98.3	116	7	ABW01705	Abw01705 Human VAM
30	170	98.3	116	7	ADG89011	Adg89011 Bovine sy
31	170	98.3	116	8	ADM97006	Adm97006 Mouse VAM
32	170	98.3	116	8	ADM97007	Adm97007 Bovine VA
33	170	98.3	116	8	ADM97005	Adm97005 Human VAM
34	170	98.3	368	3	AAY43843	Aay43843 Amino aci
35	170	98.3	368	7	ADF90403	Adf90403 Rat VAMP-
36	170	98.3	608	3	AAY43845	Aay43845 Amino aci
37	170	98.3	609	7	ADF90406	Adf90406 Rat VAMP-
38	169	97.7	35	5	AAO15158	Aao15158 Clostridi
39	168	97.1	82	3	AAY88244	Aay88244 Xenopus s
40	168	97.1	82	7	ADG89012	Adg89012 Xenopus s
41	168	97.1	114	7	ABW01720	Abw01720 Frog VAMP
42	168	97.1	114	8	ADM97008	Adm97008 Frog VAMP
43	165	95.4	35	2	AAR86824	Aar86824 VAMP isof
44	165	95.4	100	2	AAW04182	Aaw04182 Cellubrev
45	165	95.4	100	3	AAY88240	Aay88240 Human cel

ALIGNMENTS

RESULT 1
AAR86822
ID AAR86822 standard; peptide; 37 AA.
XX
AC AAR86822;
XX
DT 15-AUG-1996 (first entry)
XX
DE VAMP isoform-1 residues 60-94 (plus N- and C-terminal cysteines).
XX
KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;
KW antibody; detection; assay.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label= N-terminal Cysteine
FT /note= "may be present to attach peptide to solid-phase"
FT Peptide 2. .36
FT /note= "VAMP isoform-1 residues 60-94"
FT Misc-difference 37
FT /label= C-terminal cysteine
FT /note= "may be present to attach to peptide to solid-
FT phase"
XX
PN WO9533850-A1.
XX
PD 14-DEC-1995.
XX
PF 02-JUN-1995; 95WO-GB001279.
XX
PR 03-JUN-1994; 94GB-00011138.
XX
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX
PI Shone CC, Hallis B, James BAF, Quinn CP;
XX
DR WPI; 1996-040249/04.
XX
PT Assay for botulinum or tetanus toxin - by combining test cpd. with
PT substrate which is cleaved by the toxin, and antibody specific for the
PT cleaved but not uncleaved substrate.
XX
PS Example 1; Page 28-29; 48pp; English.
XX

CC The botulinum neurotoxins possess highly specific zinc-endopeptidase
CC activities within their light sub-units. Depending on the neurotoxin type
CC these act to cleave small proteins within the nerve cell which are
CC involved in neurotransmitter release. Antibodies are used in assays which
CC detect cleaved but not uncleaved substrate. An assay for botulinum type B
CC uses the present sequence as a substrate. It is VAMP (vesicle- associated
CC membrane protein) isoform-1, residues 60-94. The VAMP peptide can be
CC attached by a C- or N-terminal cysteine to a solid phase
XX
SQ Sequence 37 AA;

Query Match 98.3%; Score 170; DB 2; Length 37;
Best Local Similarity 94.3%; Pred. No. 4.8e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || |||||||||||||||
Db 2 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 36

RESULT 2
AAB50301
ID AAB50301 standard; peptide; 40 AA.
XX
AC AAB50301;
XX
DT 08-MAR-2001 (first entry)
XX
DE VAMP2 peptide.
XX
KW VAMP2; antibacterial; Botulinum toxin inhibitor; BttxB; previn;
KW tetanus neurotoxin; buforinin.
XX
OS Unidentified.
XX
PN WO200069891-A2.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-US013215.
XX
PR 17-MAY-1999; 99US-0134446P.
XX
PA (USSA) US DEPT OF THE ARMY.
XX
PI Gordon RK, Moorad DR, Doctor BP, Garcia GE;
XX
DR WPI; 2001-025001/03.
XX
PT Novel Previn compounds useful for inhibiting the protease activity of
PT Botulinum B and tetanus toxins.
XX
PS Disclosure; Page 5; 47pp; English.
XX
CC The present sequence was investigated in the search for Botulinum toxin
CC inhibitors (BttxB). Previn compounds which inhibit the enzymatic activity
CC of BttxB and tetanus neurotoxins were isolated. Previns may be used to
CC construct compounds such as buforinins
XX
SQ Sequence 40 AA;

Query Match 98.3%; Score 170; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 5.2e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || |||||||||||||||
Db 6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40

RESULT 3
AAB48582
ID AAB48582 standard; peptide; 40 AA.
XX
AC AAB48582;
XX
DT 08-MAR-2001 (first entry)
XX
DE VAMP2 peptide.
XX
KW Buforin; Botulinum toxin B; BttxB; Tetanus neurotoxin; endoprotease;
KW antibacterial; VAMP2; synaptobrevin.
XX
OS Unidentified.
XX
PN WO200069895-A2.
XX
PD 23-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US012909.
XX
PR 14-MAY-1999; 99US-0134216P.
XX
PA (USSA) US DEPT OF THE ARMY.
XX
PI Garcia GE, Gordon RK, Moorad DR, Doctor BP;
XX
DR WPI; 2001-102250/11.
XX
PT Novel peptides capable of inhibiting the enzymatic activity of Botulinum
PT toxin B, and Tetanus neurotoxins useful for preventing or treating toxic
PT poisoning such as Botulinum toxin and tetanus poisoning.
XX
PS Disclosure; Page 5; 47pp; English.
XX
CC The present sequence is one of a number of peptide or peptide-like
CC compounds, designated buforins, which inhibit the enzymatic activity of
CC Botulinum toxin B (BttxB) and Tetanus neurotoxins. The buforins are
CC useful for treating Botulinum or tetanus intoxication by administering a
CC composition comprising a buforin to the subject prior to the contact with
CC BttxB or tetanus intoxication. Antibodies specific for buforins are
CC useful for detecting buforins by forming immunocomplexes. The buforins
CC have improved circulatory half-life, solubility, resistance to
CC degradation and interaction with the active site of the toxin
XX
SQ Sequence 40 AA;

Query Match 98.3%; Score 170; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 5.2e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || |||||||||||||||
Db 6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40

RESULT 4
AAO15163
ID AAO15163 standard; peptide; 42 AA.
XX
AC AAO15163;
XX
DT 02-SEP-2002 (first entry)
XX
DE Clostridial neurotoxin protease substrate peptide 2.
XX
KW Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
KW fluorescence resonant energy transfer assay; quenched-signal;
KW clostridial neurotoxin detection; food.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-fluoresceinyl-glycine"
FT Cleavage-site 20. .21

FT /note= "The peptide is cleaved between these two residues
FT by the clostridial neurotoxin"
XX
PN WO200225284-A2.
XX
PD 28-MAR-2002.
XX
PF 25-SEP-2001; 2001WO-US030188.
XX
PR 25-SEP-2000; 2000US-0235050P.
XX
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Schmidt JJ, Stafford RG;
XX
DR WPI; 2002-499829/53.
XX
PT Substrate useful in e.g. an assay for the protease activity of
PT clostridial neurotoxin, comprises modified peptide or protein.
XX
PS Claim 24; Page 15; 48pp; English.
XX
CC The invention comprises clostridial neurotoxin substrate peptides which
CC can serve as fluorescence resonant energy transfer assay (FRET) or
CC quenched-signal substrates in assays for the proteolytic activities of
CC clostridial neurotoxins. The invention further comprises Clostridium
CC botulinum neurotoxin substrate peptides that can serve as immobilised
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
CC activities of clostridial neurotoxins. The clostridial (including the
CC Clostridium botulinum) neurotoxin substrate peptides are useful for
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
CC or an environmental sample). The present amino acid sequence represents a
CC clostridial neurotoxin substrate peptide of the invention
XX
SQ Sequence 42 AA;

Query Match 98.3%; Score 170; DB 5; Length 42;
Best Local Similarity 94.3%; Pred. No. 5.5e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38

RESULT 5
AAB39482
ID AAB39482 standard; protein; 54 AA.
XX
AC AAB39482;
XX
DT 02-FEB-2001 (first entry)
XX
DE Gene 49 human secreted protein homologous amino acid sequence #141.
XX
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; gene therapy;
KW food additive; preservative; chromosome identification; cancer;
KW female reproductive system disorder; immune disorder; wound healing;
KW cardiovascular disorder; neurological disease; infectious disease;
KW infection.
XX
OS Bos taurus.
XX
PN WO200058340-A2.
XX
PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US007724.
XX
PR 26-MAR-1999; 99US-0126510P.
PR 07-JAN-2000; 2000US-0174850P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-594638/56.
XX
PT Fifty nucleic acid molecules encoding human secreted proteins, useful in
PT the prevention, treatment and diagnosis of cancer, immune disorders,
PT cardiovascular disorders and neurological diseases.
XX
PS Disclosure; Page 390; 391pp; English.
XX
CC The polynucleotide sequences given in AAC74337 to AAC74386 encode the
CC human secreted proteins given in AAB39402 to AAB39451. AAB39452 to
CC AAB39484 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
CC antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
CC vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and
CC cardiant. The polynucleotides and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides
CC can also be used as a food additive or preservative to increase or
CC decrease storage capabilities. The polynucleotide are useful for
CC chromosome identification. They are also useful as probes for diagnosing
CC a disorder related to the female reproductive system, particularly breast
CC and/or ovary cancer. They are also useful in the gene therapy of breast
CC and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies,
CC agonists and antagonists are useful in the diagnosis, treatment and
CC prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular
CC disorders; (d) wound healing; (e) neurological diseases; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 54 AA;

Query Match 98.3%; Score 170; DB 3; Length 54;
Best Local Similarity 94.3%; Pred. No. 7.3e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 20 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 54

RESULT 6
AAR86821
ID AAR86821 standard; peptide; 62 AA.
XX
AC AAR86821;
XX
DT 15-AUG-1996 (first entry)
XX
DE VAMP isoform-1 residues 33-94.
XX
KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;
KW antibody; detection; assay.
XX
OS Synthetic.
XX
PN WO9533850-A1.
XX
PD 14-DEC-1995.
XX
PF 02-JUN-1995; 95WO-GB001279.
XX
PR 03-JUN-1994; 94GB-00011138.

XX
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX
PI Shone CC, Hallis B, James BAF, Quinn CP;
XX
DR WPI; 1996-040249/04.
XX
PT Assay for botulinum or tetanus toxin - by combining test cpd. with
PT substrate which is cleaved by the toxin, and antibody specific for the
PT cleaved but not uncleaved substrate.
XX
PS Example 3; Page 28; 48pp; English.
XX
CC The botulinum neurotoxins possess highly specific zinc-endopeptidase
CC activities within their light sub-units. Depending on the neurotoxin type
CC these act to cleave small proteins within the nerve cell which are
CC involved in neurotransmitter release. Antibodies are used in assays which
CC detect cleaved but not uncleaved substrate. Tetanus toxin cleaves the
CC protein VAMP (vesicle-associated membrane protein) at an identical site
CC to that of botulinum toxin type B (BoNT/B). The specificities of the
CC endopeptidase activities of the two toxins however differ in the minimum
CC peptide substrate size required for cleavage. While BoNT/B requires
CC peptide substrates of 30-35 residues in length for optimal cleavage, the
CC requirement for tetanus toxin is peptide substrates of >50 residues in
CC length. The present sequence, VAMP isoform-1 residues 33-94, is a
CC suitable substrate for tetanus toxin
XX
SQ Sequence 62 AA;

Query Match 98.3%; Score 170; DB 2; Length 62;
Best Local Similarity 94.3%; Pred. No. 8.6e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 28 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 62

RESULT 7
ADE57598
ID ADE57598 standard; protein; 115 AA.
XX
AC ADE57598;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 3460.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 8
ADE57612
ID ADE57612 standard; protein; 115 AA.
XX
AC ADE57612;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3474.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;

XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 9
ADE60831
ID ADE60831 standard; protein; 115 AA.
XX
AC ADE60831;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 6743.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 10
ADE57606
ID ADE57606 standard; protein; 115 AA.
XX
AC ADE57606;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 3468.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX

PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || |||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 11
ADE60829
ID ADE60829 standard; protein; 115 AA.
XX
AC ADE60829;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 6741.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX

PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || |||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 12
ADE57600
ID ADE57600 standard; protein; 115 AA.
XX
AC ADE57600;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3462.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || ||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 13
ADE57604
ID ADE57604 standard; protein; 115 AA.
XX
AC ADE57604;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3466.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || ||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 14
ADE57596
ID ADE57596 standard; protein; 115 AA.

XX
AC ADE57596;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3458.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

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  Query Match             98.3%;  Score 170;  DB 7;  Length 115;
  Best Local Similarity   94.3%;  Pred. No. 1.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||  || ||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
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RESULT 15
ADE57602
ID ADE57602 standard; protein; 115 AA.
XX
AC ADE57602;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 3464.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
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CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

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  Query Match             98.3%;  Score 170;  DB 7;  Length 115;
  Best Local Similarity   94.3%;  Pred. No. 1.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
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Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
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Search completed: November 1, 2004, 18:04:03
Job time : 90 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 23.4375 Seconds
(without alignments)
99.035 Million cell updates/sec

Title: US-10-802-574-4
Perfect score: 173
Sequence: 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	98.3	35	2	US-08-760-001-9	Sequence 9, Appli
2	170	98.3	35	2	US-08-760-001-11	Sequence 11, Appl
3	170	98.3	35	3	US-09-015-960-9	Sequence 9, Appli
4	170	98.3	35	3	US-09-015-960-11	Sequence 11, Appl
5	170	98.3	35	3	US-09-534-572-9	Sequence 9, Appli
6	170	98.3	35	3	US-09-534-572-11	Sequence 11, Appl
7	170	98.3	40	4	US-09-570-022-16	Sequence 16, Appl
8	170	98.3	40	4	US-09-570-023-8	Sequence 8, Appli
9	170	98.3	42	4	US-09-962-360B-9	Sequence 9, Appli
10	170	98.3	62	2	US-08-760-001-8	Sequence 8, Appli
11	170	98.3	62	3	US-09-015-960-8	Sequence 8, Appli
12	170	98.3	62	3	US-09-534-572-8	Sequence 8, Appli
13	170	98.3	116	1	US-08-409-373B-4	Sequence 4, Appli
14	170	98.3	116	1	US-08-409-373B-4	Sequence 4, Appli
15	170	98.3	116	1	US-08-393-985-16	Sequence 16, Appl
16	170	98.3	116	3	US-08-621-018B-10	Sequence 10, Appl
17	170	98.3	116	3	US-08-819-286-2	Sequence 2, Appli
18	170	98.3	116	4	US-09-483-665-10	Sequence 10, Appl
19	169	97.7	35	4	US-09-962-360B-4	Sequence 4, Appli
20	168	97.1	82	3	US-08-621-018B-11	Sequence 11, Appl
21	168	97.1	82	4	US-09-483-665-11	Sequence 11, Appl
22	165	95.4	100	3	US-08-621-018B-6	Sequence 6, Appli
23	165	95.4	100	4	US-09-483-665-6	Sequence 6, Appli
24	165	95.4	103	1	US-08-409-373B-3	Sequence 3, Appli
25	165	95.4	103	1	US-08-409-373B-3	Sequence 3, Appli
26	165	95.4	103	3	US-08-621-018B-9	Sequence 9, Appli
27	165	95.4	103	4	US-09-483-665-9	Sequence 9, Appli
28	165	95.4	118	1	US-08-393-985-14	Sequence 14, Appl
29	165	95.4	347	4	US-09-513-783A-28	Sequence 28, Appl
30	165	95.4	347	4	US-09-430-656-30	Sequence 30, Appl
31	165	95.4	350	4	US-09-513-783A-30	Sequence 30, Appl
32	165	95.4	350	4	US-09-430-656-28	Sequence 28, Appl
33	162	93.6	35	4	US-09-962-360B-3	Sequence 3, Appli
34	106	61.3	56	3	US-08-819-286-5	Sequence 5, Appli
35	93	53.8	94	4	US-09-621-976-6274	Sequence 6274, Ap
36	82	47.4	20	3	US-08-819-286-13	Sequence 13, Appl
37	82	47.4	71	4	US-09-621-976-5656	Sequence 5656, Ap
38	82	47.4	86	4	US-09-513-999C-5451	Sequence 5451, Ap
39	82	47.4	102	1	US-08-409-373B-2	Sequence 2, Appli
40	82	47.4	102	1	US-08-409-373B-2	Sequence 2, Appli
41	82	47.4	102	3	US-08-621-018B-2	Sequence 2, Appli
42	82	47.4	102	4	US-09-483-665-2	Sequence 2, Appli
43	76	43.9	141	3	US-08-621-018B-8	Sequence 8, Appli
44	76	43.9	141	4	US-09-483-665-8	Sequence 8, Appli
45	75	43.4	46	4	US-09-962-360B-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-760-001-9
; Sequence 9, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-760-001-9

Query Match 98.3%; Score 170; DB 2; Length 35;
Best Local Similarity 94.3%; Pred. No. 3.7e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db          1 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 35


RESULT 2
US-08-760-001-11
; Sequence 11, Application US/08760001
; Patent No. 5962637
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/760,001
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-760-001-11

  Query Match             98.3%;  Score 170;  DB 2;  Length 35;
  Best Local Similarity   94.3%;  Pred. No. 3.7e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db          1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35


RESULT 3
US-09-015-960-9
; Sequence 9, Application US/09015960
; Patent No. 6043042
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/015,960
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-015-960-9

  Query Match             98.3%;  Score 170;  DB 3;  Length 35;
  Best Local Similarity   94.3%;  Pred. No. 3.7e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db          1 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 35


RESULT 4
US-09-015-960-11
; Sequence 11, Application US/09015960
; Patent No. 6043042
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/015,960
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Esmond, Robert W.
;       REGISTRATION NUMBER:  32,893
;       REFERENCE/DOCKET NUMBER:  1581.0120001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2543
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  35 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-015-960-11

  Query Match             98.3%;  Score 170;  DB 3;  Length 35;
  Best Local Similarity   94.3%;  Pred. No. 3.7e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||||
Db          1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35


RESULT 5
US-09-534-572-9
; Sequence 9, Application US/09534572
; Patent No. 6337386
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/534,572
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/015,960
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:  30-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-534-572-9

  Query Match             98.3%;  Score 170;  DB 3;  Length 35;
  Best Local Similarity   94.3%;  Pred. No. 3.7e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||||
Db          1 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 35


RESULT 6
US-09-534-572-11
; Sequence 11, Application US/09534572
; Patent No. 6337386
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/534,572
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/015,960
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:  30-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-534-572-11

  Query Match             98.3%;  Score 170;  DB 3;  Length 35;
  Best Local Similarity   94.3%;  Pred. No. 3.7e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||||
Db          1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35
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RESULT 7
US-09-570-022-16
; Sequence 16, Application US/09570022
; Patent No. 6573244
; GENERAL INFORMATION:
;  APPLICANT: GORDON, RICHARD K.
;  APPLICANT:  MOORAD, DEBORAH R.
;  APPLICANT:  DOCTOR, BHUPENDRA P.
;  APPLICANT:  GARCIA, GREGORY E.
;  TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
;  TITLE OF INVENTION:  FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
;  FILE REFERENCE: 38644-170531
;  CURRENT APPLICATION NUMBER: US/09/570,022
;  CURRENT FILING DATE:  2000-05-12
;  PRIOR APPLICATION NUMBER: 60/134,446
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-570-022-16

  Query Match             98.3%;  Score 170;  DB 4;  Length 40;
  Best Local Similarity   94.3%;  Pred. No. 4.3e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db          6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40


RESULT 8
US-09-570-023-8
; Sequence 8, Application US/09570023
; Patent No. 6713444
; GENERAL INFORMATION:
;  APPLICANT: GARCIA, GREGORY E.
;  APPLICANT:  GORDON, RICHARD K.
;  APPLICANT:  MOORAD, DEBBIE R.
;  APPLICANT:  DOCTOR, BHUPENDRA P.
;  TITLE OF INVENTION: BUFORIN I AS A SPECIFIC INHIBITOR AND THERAPEUTIC AGENT
;  TITLE OF INVENTION:  FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
;  FILE REFERENCE: 37833-20004.00
;  CURRENT APPLICATION NUMBER: US/09/570,023
;  CURRENT FILING DATE:  2000-05-12
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: VAMP2
US-09-570-023-8

  Query Match             98.3%;  Score 170;  DB 4;  Length 40;
  Best Local Similarity   94.3%;  Pred. No. 4.3e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db          6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40


RESULT 9
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
;   /9
;  APPLICANT: Schmidt, James J.
;  APPLICANT:  Stafford, Robert G.
;  TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
;  TITLE OF INVENTION:  Neurotoxins
;  FILE REFERENCE: 003/224/SAP
;  CURRENT APPLICATION NUMBER: US/09/962,360B
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/235,050
;  PRIOR FILING DATE: 2001-09-25
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
;   LENGTH: 42
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1
;   OTHER INFORMATION: Xaa at 1 is N-flurescinyl-glycine
US-09-962-360B-9

  Query Match             98.3%;  Score 170;  DB 4;  Length 42;
  Best Local Similarity   94.3%;  Pred. No. 4.6e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38


RESULT 10
US-08-760-001-8
; Sequence 8, Application US/08760001
; Patent No. 5962637
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/760,001
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 amino acids
;      TYPE:  amino acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-760-001-8

  Query Match             98.3%;  Score 170;  DB 2;  Length 62;
  Best Local Similarity   94.3%;  Pred. No. 7.1e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db         28 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 62


RESULT 11
US-09-015-960-8
; Sequence 8, Application US/09015960
; Patent No. 6043042
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/015,960
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-015-960-8

  Query Match             98.3%;  Score 170;  DB 3;  Length 62;
  Best Local Similarity   94.3%;  Pred. No. 7.1e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db         28 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 62


RESULT 12
US-09-534-572-8
; Sequence 8, Application US/09534572
; Patent No. 6337386
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/534,572
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/015,960
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/760,001
;      FILING DATE:  30-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-534-572-8

  Query Match             98.3%;  Score 170;  DB 3;  Length 62;
  Best Local Similarity   94.3%;  Pred. No. 7.1e-19;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db         28 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 62


RESULT 13
US-08-409-373B-4
; Sequence 4, Application US/08409373B
; Patent No. 5585240
;  GENERAL INFORMATION:
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  CELLUBREVIN HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
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;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/409,373B
;       FILING DATE:  23-MAR-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Luther, Barbara J
;       REGISTRATION NUMBER:  33,954
;       REFERENCE/DOCKET NUMBER:  PF-0029 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-852-0195
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  116 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  X76199
US-08-409-373B-4

  Query Match             98.3%;  Score 170;  DB 1;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.5e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 14
US-08-409-373B-4
; Sequence 4, Application US/08409373B
; Patent No. 5650280
; Patent No. 5650280 5585240
;  GENERAL INFORMATION:
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  CELLUBREVIN HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/409,373B
;      FILING DATE:  23-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0029 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  116 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  X76199
US-08-409-373B-4

  Query Match             98.3%;  Score 170;  DB 1;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.5e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 15
US-08-393-985-16
; Sequence 16, Application US/08393985
; Patent No. 5693476
;  GENERAL INFORMATION:
;    APPLICANT:  Scheller, Richard H.
;    TITLE OF INVENTION:  Methods and Compositions for Modulation
;    TITLE OF INVENTION:  of Vesicular Release
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/393,985
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  8600-0152
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  116 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-393-985-16

  Query Match             98.3%;  Score 170;  DB 1;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 1.5e-18;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


Search completed: November  1, 2004, 18:19:41
Job time : 23.4375 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 69.0625 Seconds
(without alignments)
164.308 Million cell updates/sec

Title: US-10-802-574-4
Perfect score: 173
Sequence: 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	98.3	42	10	US-09-962-360B-9	Sequence 9, Appli
2	170	98.3	116	10	US-09-942-024-4	Sequence 4, Appli
3	170	98.3	116	10	US-09-942-024-17	Sequence 17, Appl
4	170	98.3	116	10	US-09-942-024-18	Sequence 18, Appl
5	170	98.3	116	10	US-09-942-098-4	Sequence 4, Appli
6	170	98.3	116	10	US-09-942-098-17	Sequence 17, Appl
7	170	98.3	116	10	US-09-942-098-18	Sequence 18, Appl
8	170	98.3	116	14	US-10-357-028-10	Sequence 10, Appl
9	170	98.3	116	15	US-10-261-161-11	Sequence 11, Appl
10	170	98.3	116	15	US-10-261-161-12	Sequence 12, Appl
11	170	98.3	116	15	US-10-261-161-13	Sequence 13, Appl
12	170	98.3	607	10	US-09-293-670-55	Sequence 55, Appl
13	169	97.7	35	10	US-09-962-360B-4	Sequence 4, Appli
14	168	97.1	82	14	US-10-357-028-11	Sequence 11, Appl
15	168	97.1	114	10	US-09-942-024-19	Sequence 19, Appl
16	168	97.1	114	10	US-09-942-098-19	Sequence 19, Appl
17	168	97.1	114	15	US-10-261-161-14	Sequence 14, Appl
18	165	95.4	100	14	US-10-357-028-6	Sequence 6, Appli
19	165	95.4	103	14	US-10-357-028-9	Sequence 9, Appli
20	165	95.4	117	16	US-10-467-595-27	Sequence 27, Appl
21	165	95.4	118	10	US-09-942-024-96	Sequence 96, Appl
22	165	95.4	118	10	US-09-942-098-96	Sequence 96, Appl
23	165	95.4	118	15	US-10-261-161-10	Sequence 10, Appl
24	165	95.4	347	14	US-10-100-957A-28	Sequence 28, Appl
25	165	95.4	350	14	US-10-100-957A-30	Sequence 30, Appl
26	165	95.4	365	10	US-09-293-670-52	Sequence 52, Appl
27	162	93.6	35	10	US-09-962-360B-3	Sequence 3, Appli
28	153	88.4	109	14	US-10-369-493-6364	Sequence 6364, Ap
29	150	86.7	40	10	US-09-942-024-57	Sequence 57, Appl
30	150	86.7	40	10	US-09-942-024-58	Sequence 58, Appl
31	150	86.7	40	10	US-09-942-024-59	Sequence 59, Appl
32	150	86.7	40	10	US-09-942-024-60	Sequence 60, Appl
33	150	86.7	40	10	US-09-942-024-61	Sequence 61, Appl
34	150	86.7	40	10	US-09-942-024-65	Sequence 65, Appl
35	150	86.7	40	10	US-09-942-098-57	Sequence 57, Appl
36	150	86.7	40	10	US-09-942-098-58	Sequence 58, Appl
37	150	86.7	40	10	US-09-942-098-59	Sequence 59, Appl
38	150	86.7	40	10	US-09-942-098-60	Sequence 60, Appl
39	150	86.7	40	10	US-09-942-098-61	Sequence 61, Appl
40	150	86.7	40	10	US-09-942-098-65	Sequence 65, Appl
41	150	86.7	40	15	US-10-261-161-82	Sequence 82, Appl
42	150	86.7	40	15	US-10-261-161-83	Sequence 83, Appl
43	150	86.7	40	15	US-10-261-161-84	Sequence 84, Appl
44	150	86.7	40	15	US-10-261-161-85	Sequence 85, Appl
45	150	86.7	40	15	US-10-261-161-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-flureseinyl-glycine
US-09-962-360B-9

Query Match 98.3%; Score 170; DB 10; Length 42;
Best Local Similarity 94.3%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
|||||||||||||||||| || ||||||||||||||||||
Db 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38

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RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-4

  Query Match             98.3%;  Score 170;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-17

  Query Match             98.3%;  Score 170;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-942-024-18

  Query Match             98.3%;  Score 170;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-4

  Query Match             98.3%;  Score 170;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-17

  Query Match             98.3%;  Score 170;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 7
US-09-942-098-18
; Sequence 18, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Clostridial
;  TITLE OF INVENTION:  Toxins
;  FILE REFERENCE: P-AR 4802
;  CURRENT APPLICATION NUMBER: US/09/942,098
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-942-098-18

  Query Match             98.3%;  Score 170;  DB 10;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 8
US-10-357-028-10
; Sequence 10, Application US/10357028
; Publication No. US20030180931A1
;   GENERAL INFORMATION:
;        APPLICANT: Stuart, Susan G.
;                   Hawkins, Phillip R.
;                   Seilhamer, Jeffrey J.
;                   Murry, Lynn E.
;        TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
;        NUMBER OF SEQUENCES: 51
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Incyte Pharmaceuticals, Inc.
;             STREET: 3174 Porter Drive
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: U.S.
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 1.5
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/357,028
;             FILING DATE: 29-Jan-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/483,665
;             FILING DATE: Herewith
;             APPLICATION NUMBER: 08/621,018
;             FILING DATE: March 22, 1996
;             APPLICATION NUMBER: 08/409,373
;             FILING DATE: March 23, 1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hamlet-Cox, Diana
;             REGISTRATION NUMBER: 33,302
;             REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-855-0555
;             TELEFAX: 650-849-8886
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 116 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        IMMEDIATE SOURCE:
;             LIBRARY: GENBANK
;             CLONE: GI 433075
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-357-028-10

  Query Match             98.3%;  Score 170;  DB 14;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 9
US-10-261-161-11
; Sequence 11, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
;  APPLICANT: Fernandez-Salas, Ester
;  APPLICANT:  Steward, Lance E.
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
;  TITLE OF INVENTION:  Transfer (FRET) Assays For Clostridial Toxins
;  FILE REFERENCE: P-AR 4804
;  CURRENT APPLICATION NUMBER: US/10/261,161
;  CURRENT FILING DATE:  2002-09-27
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-261-161-11

  Query Match             98.3%;  Score 170;  DB 15;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 7.7e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 10
US-10-261-161-12
; Sequence 12, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
;  APPLICANT: Fernandez-Salas, Ester
;  APPLICANT:  Steward, Lance E.
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
;  TITLE OF INVENTION:  Transfer (FRET) Assays For Clostridial Toxins
;  FILE REFERENCE: P-AR 4804
;  CURRENT APPLICATION NUMBER: US/10/261,161
;  CURRENT FILING DATE:  2002-09-27
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 116
;   TYPE: PRT
```

; ORGANISM: Mus musculus
US-10-261-161-12

Query Match 98.3%; Score 170; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 11
US-10-261-161-13
; Sequence 13, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-261-161-13

Query Match 98.3%; Score 170; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 12
US-09-293-670-55
; Sequence 55, Application US/09293670
; Publication No. US20030190684A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Joseph
; APPLICANT: Lorens, James
; APPLICANT: Payan, Donald
; APPLICANT: Rossi, Alexander
; TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in
; TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule
; TITLE OF INVENTION: Libraries
; FILE REFERENCE: A68104/DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/293,670
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-293-670-55

Query Match 98.3%; Score 170; DB 10; Length 607;
Best Local Similarity 94.3%; Pred. No. 4.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 61 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 95

RESULT 13
US-09-962-360B-4
; Sequence 4, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 17 and 20
; OTHER INFORMATION: Xaa at 17 is N(epsilon)-2,4-(dinitrophenyl)-lysine and Xaa at 20 i
; OTHER INFORMATION: dimethylamino-4-methyl-coumarin-3-carboxamidomethyl)-cysteine
US-09-962-360B-4

Query Match 97.7%; Score 169; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.1e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35

RESULT 14
US-10-357-028-11
; Sequence 11, Application US/10357028
; Publication No. US20030180931A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; Hawkins, Phillip R.
; Seilhamer, Jeffrey J.
; Murry, Lynn E.
; TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/357,028
; FILING DATE: 29-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/483,665
; FILING DATE: Herewith
; APPLICATION NUMBER: 08/621,018
; FILING DATE: March 22, 1996

; APPLICATION NUMBER: 08/409,373
; FILING DATE: March 23, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-Cox, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-849-8886
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 606978
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-357-028-11

Query Match 97.1%; Score 168; DB 14; Length 82;
Best Local Similarity 91.4%; Pred. No. 1.1e-16;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || ||||||||||||:|
Db 26 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 60

RESULT 15
US-09-942-024-19
; Sequence 19, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-942-024-19

Query Match 97.1%; Score 168; DB 10; Length 114;
Best Local Similarity 91.4%; Pred. No. 1.5e-16;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || ||||||||||||:|
Db 58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 92

Search completed: November 1, 2004, 18:23:47
Job time : 69.0625 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 ; Search time 18.125 Seconds
(without alignments)
185.798 Million cell updates/sec

Title: US-10-802-574-4
Perfect score: 173
Sequence: 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	98.3	116	2	B38315	synaptobrevin 2 -
2	170	98.3	116	2	JN0011	synaptobrevin 2 -
3	170	98.3	116	2	B34288	synaptobrevin 2 -
4	165	95.4	103	2	S35077	cellubrevin - rat
5	165	95.4	118	2	S52747	Vamp1 protein - hu
6	165	95.4	118	2	A38315	synaptobrevin 1 -
7	165	95.4	118	2	A34288	vesicle-associated
8	165	95.4	120	2	A32146	vesicle-associated
9	155	89.6	125	2	S40153	synaptobrevin - lo
10	153	88.4	109	2	T33239	synaptobrevin SNB-
11	116	67.1	32	2	S35555	vesicle-associated
12	116	67.1	32	2	S35553	vesicle-associated
13	116	67.1	32	2	S35554	vesicle-associated
14	116	67.1	32	2	S35552	vesicle-associated
15	113	65.3	132	2	JC1522	synaptobrevin isof
16	113	65.3	152	2	JC1521	synaptobrevin isof
17	107	61.8	145	2	T21318	hypothetical prote
18	82	47.4	115	2	S62059	synaptobrevin homo
19	81	46.8	223	2	S47654	integral membrane
20	76	43.9	121	2	T39073	synaptobrevin homo
21	72	41.6	117	2	S31250	synaptobrevin homo
22	71	41.0	1237	1	GNFF42	HIV-1 retropepsin
23	66	38.2	220	2	T00801	probable synaptobr
24	62	35.8	60	2	D44088	homeotic protein H
25	62	35.8	221	2	F84741	probable synaptobr
26	60	34.7	175	2	D86180	hypothetical prote
27	57	32.9	251	2	S64927	probable membrane
28	57	32.9	663	2	H82731	glutaryl-7-ACA acy
29	56	32.4	229	2	F86180	hypothetical prote
30	56	32.4	240	2	T47589	synaptobrevin-like
31	55	31.8	102	2	S44781	C30A5.4 protein -
32	55	31.8	102	2	T24909	hypothetical prote
33	54	31.2	219	2	T04630	synaptobrevin homo
34	54	31.2	226	2	A97774	petR protein [impo
35	54	31.2	499	2	T18791	gamma-aminobutyric
36	53	30.6	259	2	A84377	cell division prot
37	53	30.6	450	2	A97740	hypothetical prote
38	53	30.6	450	2	A71678	probable response
39	52	30.1	855	2	T29775	hypothetical prote
40	52	30.1	1116	2	T42213	m-tomosyn, isoform
41	51	29.5	210	2	T16595	hypothetical prote
42	51	29.5	1882	2	S73484	hypothetical prote
43	50	28.9	251	2	AD1145	cyclase HisF homol
44	50	28.9	629	2	E64046	mismatch repair pr
45	50	28.9	958	2	S15566	pol protein - simi

ALIGNMENTS

RESULT 1
B38315
synaptobrevin 2 - human
C;Species: Homo sapiens (man)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C;Accession: B38315
R;Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A;Title: Structures and chromosomal localizations of two human genes encoding synaptobrev
A;Reference number: A38315; MUID:91009161; PMID:1976629
A;Accession: B38315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-116 <ARC>
A;Cross-references: UNIPROT:P19065; GB:M36205; GB:J05611; NID:g338630; PIDN:AAA60604.1;
C;Genetics:
A;Gene: GDB:SYB2; VAMP-2
A;Cross-references: GDB:125293; OMIM:185881
A;Map position: 17pter-17p12
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94
```

RESULT 2
JN0011
synaptobrevin 2 - bovine
N;Alternate names: SNAP receptor
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: JN0011; S36811; S32363
R;Suedhof, T.C.; Baumert, M.; Perin, M.S.; Jahn, R.
Neuron 2, 1475-1481, 1989
A;Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.
A;Reference number: A93413; MUID:90180466; PMID:2560644
A;Accession: JN0011
A;Molecule type: mRNA
A;Residues: 1-116 <SUE>
A;Cross-references: UNIPROT:P19065; GB:X76199; NID:g433075; PIDN:CAA53792.1; PID:g433076
A;Experimental source: brain
R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A;Reference number: S36811; MUID:93374072; PMID:8365494
A;Accession: S36811

A;Molecule type: mRNA
A;Residues: 'X',48-79 <HOR>
A;Experimental source: brain
R;Soellner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Geromanos, S.; Tem
Nature 362, 318-324, 1993
A;Title: SNAP receptors implicated in vesicle targeting and fusion.
A;Reference number: S32360; MUID:93205116; PMID:8455717
A;Accession: S32363
A;Molecule type: protein
A;Residues: 31-47,'X',49-55,'X',57-59;67-82 <SOE>
A;Experimental source: brain
C;Comment: This protein is an intrinsic membrane protein of small synaptic vesicles.
C;Superfamily: synaptobrevin
C;Keywords: acetylated amino end; membrane trafficking; transmembrane protein
F;2-116/Product: synaptobrevin 2 #status predicted <MAT>
F;95-114/Domain: transmembrane #status predicted <TMM>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 3
B34288
synaptobrevin 2 - rat
N;Alternate names: vesicle-associated membrane protein 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
C;Accession: B34288; S27125
R;Elferink, L.A.; Trimble, W.S.; Scheller, R.H.
J. Biol. Chem. 264, 11061-11064, 1989
A;Title: Two vesicle-associated membrane protein genes are differentially expressed in t
A;Reference number: A34288; MUID:89291844; PMID:2472388
A;Accession: B34288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <ELF>
A;Cross-references: UNIPROT:Q64357; GB:M24105; GB:J04827; NID:g207626; PIDN:AAA42321.1;
R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R
Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt
A;Reference number: S27125; MUID:93063293; PMID:1331807
A;Accession: S27125
A;Molecule type: protein
A;Residues: 77-99,'X',101 <SCH>
C;Superfamily: synaptobrevin
C;Keywords: membrane protein; membrane trafficking; synaptic vesicle

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 4
S35077
cellubrevin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S35077
R;McMahon, H.T.; Ushkaryov, Y.A.; Edelmann, L.; Link, E.; Binz, T.; Niemann, H.; Jahn, R
Nature 364, 346-349, 1993
A;Title: Cellubrevin is a ubiquitous tetanus-toxin substrate homologous to a putative sy
A;Reference number: S35077; MUID:93323976; PMID:8332193
A;Accession: S35077
A;Molecule type: mRNA
A;Residues: 1-103 <MCM>
A;Cross-references: UNIPROT:Q64271; GB:S63830; NID:g388482; PIDN:AAB27554.1; PID:g388483
C;Superfamily: synaptobrevin

Query Match 95.4%; Score 165; DB 2; Length 103;
Best Local Similarity 91.4%; Pred. No. 1.1e-16;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 47 LSELDDRADALQAGASQFETSAAKLKRKYWWKNCK 81

RESULT 5
S52747
Vamp1 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52747
R;Gough, K.H.; Verkuylen, A.; Cosgrove, L.; Frenkel, M.J.; Ward, C.W.
submitted to the EMBL Data Library, December 1994
A;Description: Isolation and sequence analysis of SNAREs from human skeletal muscle.
A;Reference number: S52747
A;Accession: S52747
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <GOU>
A;Cross-references: UNIPROT:P23763; EMBL:Z48924; NID:g758107; PIDN:CAA88760.1; PID:g7581(
C;Superfamily: synaptobrevin

Query Match 95.4%; Score 165; DB 2; Length 118;
Best Local Similarity 91.4%; Pred. No. 1.2e-16;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 62 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 96

RESULT 6
A38315
synaptobrevin 1 - human
C;Species: Homo sapiens (man)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C;Accession: A38315
R;Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A;Title: Structures and chromosomal localizations of two human genes encoding synaptobrev
A;Reference number: A38315; MUID:91009161; PMID:1976629
A;Accession: A38315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <ARC>
A;Cross-references: UNIPROT:P23763; GB:M36200; GB:J05611; NID:g338623; PIDN:AAA60603.1; I
C;Genetics:
A;Gene: GDB:SYB1; VAMP-1
A;Cross-references: GDB:125292; OMIM:185880
A;Map position: 12p-12p
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

Query Match 95.4%; Score 165; DB 2; Length 118;
Best Local Similarity 91.4%; Pred. No. 1.2e-16;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 62 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 96

RESULT 7
A34288

vesicle-associated membrane protein 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34288
R;Elferink, L.A.; Trimble, W.S.; Scheller, R.H.
J. Biol. Chem. 264, 11061-11064, 1989
A;Title: Two vesicle-associated membrane protein genes are differentially expressed in t
A;Reference number: A34288; MUID:89291844; PMID:2472388
A;Accession: A34288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <ELF>
A;Cross-references: UNIPROT:Q63666; GB:M24104; GB:J04827; NID:g207628; PIDN:AAA42322.1;
C;Superfamily: synaptobrevin
C;Keywords: membrane protein

Query Match 95.4%; Score 165; DB 2; Length 118;
Best Local Similarity 91.4%; Pred. No. 1.2e-16;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 62 LSELDDRADALQAGASVFESSAAKLKRKYWWKNCK 96

RESULT 8
A32146
vesicle-associated membrane protein 1 - Pacific electric ray
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C;Accession: A32146
R;Trimble, W.S.; Cowan, D.M.; Scheller, R.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 4538-4542, 1988
A;Title: VAMP-1: a synaptic vesicle-associated integral membrane protein.
A;Reference number: A32146; MUID:88248054; PMID:3380805
A;Accession: A32146
A;Molecule type: mRNA
A;Residues: 1-120 <TRI>
A;Cross-references: UNIPROT:P13701; EMBL:J03777; NID:g213245; PIDN:AAA49286.1; PID:g2132
C;Superfamily: synaptobrevin
C;Keywords: membrane protein

Query Match 95.4%; Score 165; DB 2; Length 120;
Best Local Similarity 91.4%; Pred. No. 1.3e-16;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 64 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 98

RESULT 9
S40153
synaptobrevin - longfin squid
C;Species: Loligo pealeii (longfin squid)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40153
R;Bommert, K.; Kistner, A.; Hasermann, E.; Betz, H.
submitted to the EMBL Data Library, August 1993
A;Description: Conservation of primary structure and clostridial neurotoxin cleavage sit
A;Reference number: S40153
A;Accession: S40153
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <BOM>
A;Cross-references: UNIPROT:P47194; EMBL:X74748; NID:g437855; PIDN:CAA52766.1; PID:g4378
C;Superfamily: synaptobrevin

Query Match 89.6%; Score 155; DB 2; Length 125;
Best Local Similarity 82.9%; Pred. No. 3.7e-15;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 69 ISELDDRADALQAGASQFEASAGKLKRKFWWKNCK 103

RESULT 10
T33239
synaptobrevin SNB-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33239
R;Greco, T.; Bradshaw, H.; O'Brien, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T10H9.
A;Reference number: Z21306
A;Accession: T33239
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-109 <GRE>
A;Cross-references: UNIPROT:O02495; EMBL:AF067949; PIDN:AAC19234.1; GSPDB:GN00023; CESP:T
A;Experimental source: strain Bristol N2; clone T10H9
C;Genetics:
A;Gene: SNB-1; CESP:T10H9.4
A;Map position: 5
A;Introns: 39/3
C;Superfamily: synaptobrevin

Query Match 88.4%; Score 153; DB 2; Length 109;
Best Local Similarity 82.9%; Pred. No. 6.3e-15;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
Db 52 LSQLDDRADALQEGASQFEKSAATLKRKYWWKNIK 86

RESULT 11
S35555
vesicle-associated membrane protein 2 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S35555
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35555
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q7LZ64
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

Query Match 67.1%; Score 116; DB 2; Length 32;
Best Local Similarity 92.6%; Pred. No. 3.9e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKR 27
Db 6 LSELDDRADALQAGASQFETSAAKLKR 32

RESULT 12
S35553
vesicle-associated membrane protein 1 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 20-May-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S35553
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35553
A;Molecule type: DNA

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A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q7LZ65
C;Superfamily: synaptobrevin

  Query Match             67.1%;  Score 116;  DB 2;  Length 32;
  Best Local Similarity   92.6%;  Pred. No. 3.9e-10;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKR 27
              |||||||||||||||| || |||||||
Db          6 LSELDDRADALQAGASVFESSAAKLKR 32


RESULT 13
S35554
vesicle-associated membrane protein 2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S35554
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35554
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:O35619
C;Superfamily: synaptobrevin

  Query Match             67.1%;  Score 116;  DB 2;  Length 32;
  Best Local Similarity   92.6%;  Pred. No. 3.9e-10;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKR 27
              |||||||||||||||| || |||||||
Db          6 LSELDDRADALQAGASQFETSAAKLKR 32


RESULT 14
S35552
vesicle-associated membrane protein 1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S35552
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35552
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q9CXX2
C;Superfamily: synaptobrevin

  Query Match             67.1%;  Score 116;  DB 2;  Length 32;
  Best Local Similarity   92.6%;  Pred. No. 3.9e-10;
  Matches   25;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKR 27
              |||||||||||||||| || |||||||
Db          6 LSELDDRADALQAGASQFESSAAKLKR 32


RESULT 15
JC1522
synaptobrevin isoform B - fruit fly (Drosophila melanogaster)
N;Alternate names: vesicle-associated membrane protein B
C;Species: Drosophila melanogaster
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: JC1522
R;Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.
Gene 131, 175-181, 1993
A;Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene
A;Reference number: JC1521; MUID:94010306; PMID:8406010
A;Accession: JC1522
A;Molecule type: DNA
A;Residues: 1-132 <CHI>
A;Cross-references: UNIPROT:P18489; GB:L14270; NID:g290281; PIDN:AAA28923.1; PID:g290282
A;Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue 1
C;Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobrev
C;Genetics:
A;Gene: syb
A;Cross-references: FlyBase:FBgn0003660
A;Introns: 16/2; 128/1
C;Superfamily: synaptobrevin
C;Keywords: membrane protein; synaptic vesicle

  Query Match             65.3%;  Score 113;  DB 2;  Length 132;
  Best Local Similarity   62.9%;  Pred. No. 4.7e-09;
  Matches   22;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||| :||| |: ||| | | ||||| || |:|
Db         76 LSELGERADQLEQGASQSEQQAGKLKRKQWWANMK 110


Search completed: November 1, 2004, 17:53:52
Job time : 19.125 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 97.1875 Seconds
(without alignments)
207.209 Million cell updates/sec

Title: US-10-802-574-4
Perfect score: 173
Sequence: 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB		Description
1	170	98.3	81	2	Q8HZX7	Q8hzx7 oryctolagus
2	170	98.3	114	2	Q6P835	Q6p835 xenopus tro
3	170	98.3	114	2	AAH61396	Aah61396 xenopus t
4	170	98.3	115	1	VAM2_HUMAN	P19065 homo sapien
5	170	98.3	115	1	VAM2_MOUSE	Q64357 mus musculu
6	170	98.3	116	2	Q9BUC2	Q9buc2 homo sapien
7	170	98.3	116	2	Q9N0Y0	Q9n0y0 macaca mula
8	170	98.3	116	2	O35619	O35619 mus musculu
9	170	98.3	116	2	AAH02737	Aah02737 homo sapi
10	170	98.3	116	2	AAH55105	Aah55105 mus muscu
11	170	98.3	116	2	BAC41125	Bac41125 mus muscu
12	170	98.3	135	2	Q9WUW2	Q9wuw2 rattus norv
13	170	98.3	142	2	Q8CHR4	Q8chr4 mus musculu
14	168	97.1	113	1	VAM2_XENLA	P47193 xenopus lae
15	168	97.1	114	2	AAH60344	Aah60344 xenopus l
16	165	95.4	99	1	VAM3_HUMAN	Q15836 homo sapien
17	165	95.4	103	1	VAM3_MOUSE	Q64271 mus musculu
18	165	95.4	103	2	AAG42468	Aag42468 mus muscu
19	165	95.4	103	2	AAH60045	Aah60045 mus muscu
20	165	95.4	103	2	BAC34586	Bac34586 mus muscu
21	165	95.4	103	2	BAC34723	Bac34723 mus muscu
22	165	95.4	116	2	Q8CH14	Q8ch14 rattus norv
23	165	95.4	117	2	Q8IVC9	Q8ivc9 homo sapien
24	165	95.4	117	2	O09025	O09025 rattus norv
25	165	95.4	117	2	Q6PFF3	Q6pff3 mus musculu
26	165	95.4	117	2	AAH57587	Aah57587 mus muscu
27	165	95.4	118	1	VAM1_HUMAN	P23763 homo sapien
28	165	95.4	118	1	VAM1_MOUSE	Q62442 mus musculu
29	165	95.4	118	1	VAM1_RAT	Q63666 rattus norv
30	165	95.4	118	2	BAC37151	Bac37151 mus muscu
31	165	95.4	120	1	SYB_TORCA	P13701 torpedo cal
32	165	95.4	182	2	Q9CXX2	Q9cxx2 mus musculu
33	164	94.8	114	2	O57345	O57345 xenopus lae
34	163	94.2	102	2	Q6IQK3	Q6iqk3 brachydanio
35	163	94.2	102	2	AAH71402	Aah71402 brachydan
36	163	94.2	119	2	Q6PBJ3	Q6pbj3 brachydanio
37	163	94.2	119	2	AAH59687	Aah59687 brachydan
38	161	93.1	100	2	Q9BRV4	Q9brv4 homo sapien
39	160	92.5	110	2	Q7SZZ5	Q7szz5 brachydanio
40	160	92.5	110	2	AAH59626	Aah59626 brachydan
41	160	92.5	112	2	O57432	O57432 fugu rubrip
42	156	90.2	86	2	Q6DLT0	Q6dlt0 lateolabrax
43	156	90.2	110	2	Q8T897	Q8t897 halocynthia
44	156	90.2	160	2	Q86FE0	Q86fe0 schistosoma
45	155	89.6	118	2	Q6DGI1	Q6dgi1 brachydanio

ALIGNMENTS

RESULT 1
Q8HZX7
ID Q8HZX7 PRELIMINARY; PRT; 81 AA.
AC Q8HZX7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptobrevin-2 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal collecting duct;
RX PubMed=12186952;
RA Gouraud S., Laera A., Calamita G., Carmosino M., Procino G.,
RA Rossetto O., Mannucci R., Rosenthal W., Svelto M., Valenti G.;
RT "Functional involvement of VAMP/synaptobrevin-2 in cAMP-stimulated
RT aquaporin 2 translocation in renal collecting duct cells.";
RL J. Cell Sci. 115:3667-3674(2002).
DR EMBL; AF262953; AAN14408.1; -.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin; 1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; Synaptobrevin; 1.
DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR PROSITE; PS50892; V_SNARE; 1.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9357 MW; 6F171CA14775860C CRC64;

Query Match 98.3%; Score 170; DB 2; Length 81;
Best Local Similarity 94.3%; Pred. No. 6.1e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||  ||  ||||||||||||||||
Db         32 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 66
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RESULT 2
Q6P835
ID Q6P835 PRELIMINARY; PRT; 114 AA.
AC Q6P835;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75977.
GN Name=MGC75977;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.

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OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061396; AAH61396.1; -.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   114 AA;  12440 MW;  0EE3EADBDF2A1ABE CRC64;

  Query Match             98.3%;  Score 170;  DB 2;  Length 114;
  Best Local Similarity   94.3%;  Pred. No. 8.8e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 92


RESULT 3
AAH61396
ID   AAH61396    PRELIMINARY;      PRT;   114 AA.
AC   AAH61396;
DT   25-MAR-2004 (TrEMBLrel. 27, Created)
DT   25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC75977.
GN   MGC75977.
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061396; AAH61396.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   114 AA;  12440 MW;  0EE3EADBDF2A1ABE CRC64;

  Query Match             98.3%;  Score 170;  DB 2;  Length 114;
  Best Local Similarity   94.3%;  Pred. No. 8.8e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              ||||||||||||||||| || |||||||||||||||
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 92


RESULT 4
VAM2_HUMAN
ID   VAM2_HUMAN     STANDARD;      PRT;   115 AA.
AC   P19065;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).
GN   Name=VAMP2; Synonyms=SYB2;
OS   Homo sapiens (Human), and
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606, 9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human;
RX   MEDLINE=91009161; PubMed=1976629;
RA   Archer B.T. III, Oezcelik T., Jahn R., Francke U., Suedhof T.C.;
RT   "Structures and chromosomal localizations of two human genes encoding
RT   synaptobrevins 1 and 2.";
RL   J. Biol. Chem. 265:17267-17273(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human; TISSUE=Peripheral blood;
RA   Nabokina S.M., Lazo P.A., Mollinedo F.;
RT   "Expression of VAMP genes in human neutrophils.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human; TISSUE=Blood;
RA   Taruscio D., Zoraqi K.G., Falbo V.;
RT   "Genomic structure of human SYB2 gene.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Bovine;
RX   MEDLINE=90180466; PubMed=2560644;
RA   Suedhof T.C., Baumert M., Perin M.S., Jahn R.;
RT   "A synaptic vesicle membrane protein is conserved from mammals to
RT   Drosophila.";
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RL   Neuron 2:1475-1481(1989).
RN   [5]
RP   SEQUENCE OF 31-59 AND 67-82, AND ACETYLATION.
RC   SPECIES=Bovine;
RX   MEDLINE=93205116; PubMed=8455717;
RA   Soellner T., Whiteheart S.W., Brunner M., Erdjument-Bromage H.,
RA   Geromanos S., Tempst P., Rothman J.E.;
RT   "SNAP receptors implicated in vesicle targeting and fusion.";
RL   Nature 362:318-324(1993).
RN   [6]
RP   TISSUE SPECIFICITY.
RC   SPECIES=Human;
RX   MEDLINE=96332494; PubMed=8760387;
RA   Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
RA   Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
RA   Ward C.W.;
RT   "Insulin-responsive tissues contain the core complex protein SNAP-25
RT   (synaptosomal-associated protein 25) A and B isoforms in addition to
RT   syntaxin 4 and synaptobrevins 1 and 2.";
RL   Biochem. J. 317:945-954(1996).
RN   [7]
RP   TOPOLOGY.
RC   SPECIES=Human;
RX   MEDLINE=95137000; PubMed=7835332;
RA   Kutay U., Ahnert-Hilger G., Hartmann E., Wiedenmann B., Rapoport T.A.;
RT   "Transport route for synaptobrevin via a novel pathway of insertion
RT   into the endoplasmic reticulum membrane.";
RL   EMBO J. 14:217-223(1995).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-88 IN COMPLEX WITH BOTB.
RC   SPECIES=Human;
RX   MEDLINE=20392548; PubMed=10932255; DOI=10.1038/77997;
RA   Hanson M.A., Stevens R.C.;
RT   "Cocrystal structure of synaptobrevin-II bound to botulinum neurotoxin
RT   type B at 2.0 A resolution.";
RL   Nat. Struct. Biol. 7:687-692(2000).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBUNIT: Interacts with VAPA and VAPB.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- TISSUE SPECIFICITY: Nervous system and skeletal muscle.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M36205; AAA60604.1; -.
DR   EMBL; M36201; AAA60604.1; JOINED.
DR   EMBL; M36202; AAA60604.1; JOINED.
DR   EMBL; M36203; AAA60604.1; JOINED.
DR   EMBL; M36204; AAA60604.1; JOINED.
DR   EMBL; AJ225044; CAA12385.1; -.
DR   EMBL; AF135372; AAF15551.1; -.
DR   EMBL; X76199; CAA53792.1; -.
DR   PIR; B38315; B38315.
DR   PIR; JN0011; JN0011.
DR   PDB; 1F83; X-ray; B=52-75, C=76-87.
DR   Genew; HGNC:12643; VAMP2.
DR   MIM; 185881; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   3D-structure; Acetylation; Coiled coil; Direct protein sequencing;
KW   Multigene family; Synapse; Synaptosome; Transmembrane.
FT   INIT_MET      0      0
FT   DOMAIN        1     93       Cytoplasmic (Potential).
FT   TRANSMEM     94    113       Anchor for type IV membrane protein
FT                                (Potential).
FT   DOMAIN      114    115       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine.
FT   DOMAIN       30     90       v-SNARE coiled-coil homology.
SQ   SEQUENCE   115 AA;  12517 MW;  388B79F0D21AD81E CRC64;

  Query Match             98.3%;  Score 170;  DB 1;  Length 115;
  Best Local Similarity   94.3%;  Pred. No. 8.9e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || ||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93


RESULT 5
VAM2_MOUSE
ID   VAM2_MOUSE     STANDARD;      PRT;   115 AA.
AC   Q64357;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).
GN   Name=Vamp2; Synonyms=Syb2;
OS   Mus musculus (Mouse), and
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090, 10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=89291844; PubMed=2472388;
RA   Elferink L.A., Trimble W.S., Scheller R.H.;
RT   "Two vesicle-associated membrane protein genes are differentially
RT   expressed in the rat central nervous system.";
RL   J. Biol. Chem. 264:11061-11064(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Mouse;
RX   MEDLINE=98104125; PubMed=9430681;
RA   Martin L.B., Shewan A., Millar C.A., Gould G.W., James D.E.;
RT   "Vesicle-associated membrane protein 2 plays a specific role in the
RT   insulin-dependent trafficking of the facilitative glucose transporter
RT   GLUT4 in 3T3-L1 adipocytes.";
RL   J. Biol. Chem. 273:1444-1452(1998).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-96 IN COMPLEX WITH STX1A
RP   AND SNAP25.
RC   SPECIES=Rat;
RX   MEDLINE=98430524; PubMed=9759724; DOI=10.1038/26412;
RA   Sutton R.B., Fasshauer D., Jahn R., Brunger A.T.;
RT   "Crystal structure of a SNARE complex involved in synaptic exocytosis
RT   at 2.4 A resolution.";
RL   Nature 395:347-353(1998).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 29-93 IN COMPLEX WITH STX1A;
RP   CPLX1 AND SNAP25, AND NMR ANALYSIS.
RC   SPECIES=Rat;
RX   MEDLINE=21822661; PubMed=11832227;
RA   Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
RA   Suedhof T.C., Rizo J.;
RT   "Three-dimensional structure of the complexin/SNARE complex.";
RL   Neuron 33:397-409(2002).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 28-89 IN COMPLEX WITH STX1A
RP   AND SNAP25.
RC   SPECIES=Rat;
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RX   MEDLINE=22499607; PubMed=12496247; DOI=10.1074/jbc.M211889200;
RA   Ernst J.A., Brunger A.T.;
RT   "High resolution structure, stability, and synaptotagmin binding of a
RT   truncated neuronal SNARE complex.";
RL   J. Biol. Chem. 278:8630-8636(2003).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBUNIT: Interacts with VAPA and VAPB (By similarity). Part of the
CC       SNARE core complex containing SNAP25, VAMP2 and STX1A. This
CC       complex binds to CPLX1.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- TISSUE SPECIFICITY: Nervous system specific. A higher level
CC       expression is seen in the brain as compared to the spinal cord.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M24105; AAA42321.1; -.
DR   EMBL; U60150; AAB03463.1; -.
DR   PIR; B34288; B34288.
DR   PDB; 1KIL; X-ray; A=26-91.
DR   PDB; 1N7S; X-ray; A=26-88.
DR   PDB; 1SFC; X-ray; A/E/I=1-95.
DR   MGD; MGI:1313277; Vamp2.
DR   RGD; 3949; Vamp2.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   3D-structure; Acetylation; Coiled coil; Multigene family;
KW   Polymorphism; Synapse; Synaptosome; Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     93       Cytoplasmic (Potential).
FT   TRANSMEM     94    113       Anchor for type IV membrane protein
FT                                (Potential).
FT   DOMAIN      114    115       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine (By similarity).
FT   DOMAIN       30     90       v-SNARE coiled-coil homology.
FT   VARIANT     110    110       I -> II.
FT   VARIANT     111    111       V -> I.
FT   HELIX        28     87
SQ   SEQUENCE   115 AA;  12559 MW;  EA400D6291ABF0BC CRC64;

  Query Match             98.3%;  Score 170;  DB 1;  Length 115;
  Best Local Similarity   94.3%;  Pred. No. 8.9e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || ||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93


RESULT 6
Q9BUC2
ID   Q9BUC2      PRELIMINARY;      PRT;   116 AA.
AC   Q9BUC2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Vesicle-associated membrane protein 2 (Synaptobrevin 2).
GN   Name=VAMP2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, Lung, and Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002737; AAH02737.3; -.
DR   EMBL; BC019608; AAH19608.1; -.
DR   EMBL; BC033870; AAH33870.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             98.3%;  Score 170;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 9e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 7
Q9N0Y0
ID   Q9N0Y0      PRELIMINARY;      PRT;   116 AA.
AC   Q9N0Y0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   VAMP-2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hippocampus;
RA   Jensen M.J., Smith L.A.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF240769; AAF64476.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             98.3%;  Score 170;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 9e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 8
O35619
ID   O35619      PRELIMINARY;      PRT;   116 AA.
AC   O35619;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vesicle associated membrane protein 2.
GN   Name=Vamp2; Synonyms=mVAMP-2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Olken S.K., Doerre S., Corley R.B.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF007168; AAB62931.1; -.
DR   PIR; S35554; S35554.
DR   HSSP; Q9WUW2; 1SFC.
DR   MGD; MGI:1313277; Vamp2.
DR   GO; GO:0030141; C:secretory granule; IDA.
DR   GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR   GO; GO:0042589; C:zymogen granule membrane; IDA.
DR   GO; GO:0005516; F:calmodulin binding; IDA.
DR   GO; GO:0005543; F:phospholipid binding; IDA.
DR   GO; GO:0000149; F:SNARE binding; IDA.
DR   GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.
DR   GO; GO:0017157; P:regulation of exocytosis; IDA.
DR   GO; GO:0016083; P:synaptic vesicle fusion; IMP.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12677 MW;  4E1D0D56B5409D0A CRC64;

  Query Match             98.3%;  Score 170;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 9e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 9
AAH02737
ID   AAH02737    PRELIMINARY;      PRT;   116 AA.
AC   AAH02737;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Vesicle-associated membrane protein 2 (Synaptobrevin 2).
GN   VAMP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002737; AAH02737.3; -.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             98.3%;  Score 170;  DB 2;  Length 116;
  Best Local Similarity   94.3%;  Pred. No. 9e-17;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 10
AAH55105
ID   AAH55105    PRELIMINARY;      PRT;   116 AA.
AC   AAH55105;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Vesicle-associated membrane protein 2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC055105; AAH55105.1; -.
SQ SEQUENCE 116 AA; 12691 MW; 4A0D0D56B5409D0A CRC64;

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || |||||||||||||||
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 11
BAC41125
ID BAC41125 PRELIMINARY; PRT; 116 AA.
AC BAC41125;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE 15 days embryo brain cDNA, RIKEN full-length enriched library,
DE clone:G630012G02 product:unclassifiable, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK090178; BAC41125.1; -.
SQ SEQUENCE 116 AA; 12691 MW; 4A0D0D56B5409D0A CRC64;

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
||||||||||||||||| || |||||||||||||||
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 12
Q9WUW2
ID Q9WUW2 PRELIMINARY; PRT; 135 AA.
AC Q9WUW2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vesicle associated membrane protein 2B.
GN Name=vamp2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=99297576; PubMed=10371166;
RA Mandic R., Lowe A.W.;
RT "Characterization of an alternatively spliced isoform of rat vesicle
RT associated membrane protein-2 (VAMP-2).";
RL FEBS Lett. 451:209-213(1999).
DR EMBL; AJ133104; CAB43509.1; -.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin; 1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; Synaptobrevin; 1.

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DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   135 AA;  14509 MW;  F37D14A87BDAB1F6 CRC64;

  Query Match             98.3%;  Score 170;  DB 2;  Length 135;
  Best Local Similarity   94.3%;  Pred. No. 1.1e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || ||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 13
Q8CHR4
ID   Q8CHR4      PRELIMINARY;      PRT;   142 AA.
AC   Q8CHR4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vamp2 protein (Fragment).
GN   Name=Vamp2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA   Strausberg R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC039745; AAH39745.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   MGD; MGI:1313277; Vamp2.
DR   GO; GO:0030141; C:secretory granule; IDA.
DR   GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR   GO; GO:0042589; C:zymogen granule membrane; IDA.
DR   GO; GO:0005516; F:calmodulin binding; IDA.
DR   GO; GO:0005543; F:phospholipid binding; IDA.
DR   GO; GO:0000149; F:SNARE binding; IDA.
DR   GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.
DR   GO; GO:0017157; P:regulation of exocytosis; IDA.
DR   GO; GO:0016083; P:synaptic vesicle fusion; IMP.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   142 AA;  15313 MW;  F1B0C9C9B495B776 CRC64;

  Query Match             98.3%;  Score 170;  DB 2;  Length 142;
  Best Local Similarity   94.3%;  Pred. No. 1.1e-16;
  Matches   33;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || ||||||||||||||||
Db         86 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 120


RESULT 14
VAM2_XENLA
ID   VAM2_XENLA     STANDARD;      PRT;   113 AA.
AC   P47193;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2)
DE   (SYBII).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang X.-H., Poo M.-M.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 32-113 FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=95324415; PubMed=7601005;
RA   Knecht A.K., Good P.J., Dawid I.B., Harland R.M.;
RT   "Dorsal-ventral patterning and differentiation of noggin-induced
RT   neural tissue in the absence of mesoderm.";
RL   Development 121:1927-1935(1995).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF035017; AAB88138.1; -.
DR   EMBL; U16801; AAA81376.1; -.
DR   HSSP; P19065; 1F83.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Acetylation; Coiled coil; Multigene family; Synapse; Synaptosome;
KW   Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     91       Cytoplasmic (Potential).
FT   TRANSMEM     92    110       Anchor for type IV membrane protein
FT                                (Potential).
FT   DOMAIN      111    113       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine (By similarity).
FT   DOMAIN       28     88       v-SNARE coiled-coil homology.
SQ   SEQUENCE   113 AA;  12341 MW;  6EC6C937B29BC6AB CRC64;
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Query Match 97.1%; Score 168; DB 1; Length 113;
Best Local Similarity 91.4%; Pred. No. 1.7e-16;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
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Db         57 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 91
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RESULT 15
AAH60344
ID AAH60344 PRELIMINARY; PRT; 114 AA.
AC AAH60344;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Vamp2-B-prov protein.
GN VAMP2-B-PROV.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC060344; AAH60344.1; -.
SQ SEQUENCE 114 AA; 12472 MW; AEF2EDDCDF2D1DBF CRC64;

Query Match 97.1%; Score 168; DB 2; Length 114;
Best Local Similarity 91.4%; Pred. No. 1.7e-16;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LSELDDRADALQAGASXFEXSAAKLKRKYWWKNLK 35
              |||||||||||||||| || |||||||||||||:|
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 92
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Search completed: November 1, 2004, 17:59:09
Job time : 97.1875 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 108 Seconds
(without alignments)
139.506 Million cell updates/sec

Title: US-10-802-574-9
Perfect score: 221
Sequence: 1 XGGLSELDDRADALQAGASQ.....TSAAKLKRKYWWKNLKGGGC 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	220	99.5	42	5	AAO15163	Aao15163 Clostridi
2	181	81.9	40	4	AAB50301	Aab50301 VAMP2 pep
3	181	81.9	40	4	AAB48582	Aab48582 VAMP2 pep
4	181	81.9	54	3	AAB39482	Aab39482 Gene 49 h
5	181	81.9	115	7	ADE57598	Ade57598 Human Pro
6	181	81.9	115	7	ADE57612	Ade57612 Rat Prote
7	181	81.9	115	7	ADE60831	Ade60831 Human Pro
8	181	81.9	115	7	ADE57606	Ade57606 Human Pro
9	181	81.9	115	7	ADE60829	Ade60829 Rat Prote
10	181	81.9	115	7	ADE57600	Ade57600 Rat Prote
11	181	81.9	115	7	ADE57604	Ade57604 Rat Prote
12	181	81.9	115	7	ADE57596	Ade57596 Rat Prote
13	181	81.9	115	7	ADE57602	Ade57602 Human Pro
14	181	81.9	115	7	ADE57610	Ade57610 Human Pro
15	181	81.9	115	7	ADE57592	Ade57592 Rat Prote
16	181	81.9	115	7	ADE57594	Ade57594 Human Pro
17	181	81.9	115	7	ADE57614	Ade57614 Human Pro
18	181	81.9	115	7	ADE57608	Ade57608 Rat Prote
19	181	81.9	116	2	AAW30104	Aaw30104 Vesicle-a
20	181	81.9	116	2	AAW43425	Aaw43425 Rat vesic
21	181	81.9	116	3	AAY88243	Aay88243 Bovine sy
22	181	81.9	116	5	ABP43681	Abp43681 VAMP-2 se
23	181	81.9	116	6	ABP76220	Abp76220 Human GEN
24	181	81.9	116	6	AAE36664	Aae36664 Human VAM
25	181	81.9	116	7	ABW01719	Abw01719 Bovine VA
26	181	81.9	116	7	ABW01718	Abw01718 Mouse VAM
27	181	81.9	116	7	ABW01705	Abw01705 Human VAM
28	181	81.9	116	7	ADG89011	Adg89011 Bovine sy
29	181	81.9	116	8	ADM97006	Adm97006 Mouse VAM
30	181	81.9	116	8	ADM97007	Adm97007 Bovine VA
31	181	81.9	116	8	ADM97005	Adm97005 Human VAM
32	181	81.9	368	3	AAY43843	Aay43843 Amino aci
33	181	81.9	368	7	ADF90403	Adf90403 Rat VAMP-
34	181	81.9	608	3	AAY43845	Aay43845 Amino aci
35	181	81.9	609	7	ADF90406	Adf90406 Rat VAMP-
36	179	81.0	82	3	AAY88244	Aay88244 Xenopus s
37	179	81.0	82	7	ADG89012	Adg89012 Xenopus s
38	179	81.0	114	7	ABW01720	Abw01720 Frog VAMP
39	179	81.0	114	8	ADM97008	Adm97008 Frog VAMP
40	177	80.1	37	2	AAR86822	Aar86822 VAMP isof
41	177	80.1	62	2	AAR86821	Aar86821 VAMP isof
42	176	79.6	35	2	AAR86824	Aar86824 VAMP isof
43	176	79.6	100	2	AAW04182	Aaw04182 Cellubrev
44	176	79.6	100	3	AAY88240	Aay88240 Human cel
45	176	79.6	100	4	AAU00250	Aau00250 SNARE hom

ALIGNMENTS

RESULT 1
AAO15163
ID AAO15163 standard; peptide; 42 AA.
XX
AC AAO15163;
XX
DT 02-SEP-2002 (first entry)
XX
DE Clostridial neurotoxin protease substrate peptide 2.
XX
KW Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
KW fluorescence resonant energy transfer assay; quenched-signal;
KW clostridial neurotoxin detection; food.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-fluoresceinyl-glycine"
FT Cleavage-site 20. .21
FT /note= "The peptide is cleaved between these two residues
FT by the clostridial neurotoxin"
XX
PN WO200225284-A2.
XX
PD 28-MAR-2002.
XX
PF 25-SEP-2001; 2001WO-US030188.
XX
PR 25-SEP-2000; 2000US-0235050P.
XX
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Schmidt JJ, Stafford RG;
XX
DR WPI; 2002-499829/53.
XX
PT Substrate useful in e.g. an assay for the protease activity of
PT clostridial neurotoxin, comprises modified peptide or protein.
XX
PS Claim 24; Page 15; 48pp; English.
XX
CC The invention comprises clostridial neurotoxin substrate peptides which
CC can serve as fluorescence resonant energy transfer assay (FRET) or
CC quenched-signal substrates in assays for the proteolytic activities of
CC clostridial neurotoxins. The invention further comprises Clostridium
CC botulinum neurotoxin substrate peptides that can serve as immobilised
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic

CC activities of clostridial neurotoxins. The clostridial (including the
CC Clostridium botulinum) neurotoxin substrate peptides are useful for
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
CC or an environmental sample). The present amino acid sequence represents a
CC clostridial neurotoxin substrate peptide of the invention
XX
SQ Sequence 42 AA;

Query Match 99.5%; Score 220; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.5e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKGGGC 42
||||||||||||||||||||||||||||||||||||||||||
Db 2 GGLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKGGGC 42

RESULT 2
AAB50301
ID AAB50301 standard; peptide; 40 AA.
XX
AC AAB50301;
XX
DT 08-MAR-2001 (first entry)
XX
DE VAMP2 peptide.
XX
KW VAMP2; antibacterial; Botulinum toxin inhibitor; BttxB; previn;
KW tetanus neurotoxin; buforinin.
XX
OS Unidentified.
XX
PN WO200069891-A2.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-US013215.
XX
PR 17-MAY-1999; 99US-0134446P.
XX
PA (USSA) US DEPT OF THE ARMY.
XX
PI Gordon RK, Moorad DR, Doctor BP, Garcia GE;
XX
DR WPI; 2001-025001/03.
XX
PT Novel Previn compounds useful for inhibiting the protease activity of
PT Botulinum B and tetanus toxins.
XX
PS Disclosure; Page 5; 47pp; English.
XX
CC The present sequence was investigated in the search for Botulinum toxin
CC inhibitors (BttxB). Previn compounds which inhibit the enzymatic activity
CC of BttxB and tetanus neurotoxins were isolated. Previns may be used to
CC construct compounds such as buforinins
XX
SQ Sequence 40 AA;

Query Match 81.9%; Score 181; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
|||||||||||||||||||||||||||||||||||
Db 6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40

RESULT 3
AAB48582
ID AAB48582 standard; peptide; 40 AA.
XX
AC AAB48582;
XX
DT 08-MAR-2001 (first entry)
XX
DE VAMP2 peptide.
XX
KW Buforin; Botulinum toxin B; BttxB; Tetanus neurotoxin; endoprotease;
KW antibacterial; VAMP2; synaptobrevin.
XX
OS Unidentified.
XX
PN WO200069895-A2.
XX
PD 23-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US012909.
XX
PR 14-MAY-1999; 99US-0134216P.
XX
PA (USSA) US DEPT OF THE ARMY.
XX
PI Garcia GE, Gordon RK, Moorad DR, Doctor BP;
XX
DR WPI; 2001-102250/11.
XX
PT Novel peptides capable of inhibiting the enzymatic activity of Botulinum
PT toxin B, and Tetanus neurotoxins useful for preventing or treating toxic
PT poisoning such as Botulinum toxin and tetanus poisoning.
XX
PS Disclosure; Page 5; 47pp; English.
XX
CC The present sequence is one of a number of peptide or peptide-like
CC compounds, designated buforins, which inhibit the enzymatic activity of
CC Botulinum toxin B (BttxB) and Tetanus neurotoxins. The buforins are
CC useful for treating Botulinum or tetanus intoxication by administering a
CC composition comprising a buforin to the subject prior to the contact with
CC BttxB or tetanus intoxication. Antibodies specific for buforins are
CC useful for detecting buforins by forming immunocomplexes. The buforins
CC have improved circulatory half-life, solubility, resistance to
CC degradation and interaction with the active site of the toxin
XX
SQ Sequence 40 AA;

Query Match 81.9%; Score 181; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
|||||||||||||||||||||||||||||||||||
Db 6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40

RESULT 4
AAB39482
ID AAB39482 standard; protein; 54 AA.
XX
AC AAB39482;
XX
DT 02-FEB-2001 (first entry)
XX
DE Gene 49 human secreted protein homologous amino acid sequence #141.
XX
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; gene therapy;
KW food additive; preservative; chromosome identification; cancer;
KW female reproductive system disorder; immune disorder; wound healing;
KW cardiovascular disorder; neurological disease; infectious disease;
KW infection.
XX
OS Bos taurus.
XX
PN WO200058340-A2.
XX

PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US007724.
XX
PR 26-MAR-1999; 99US-0126510P.
PR 07-JAN-2000; 2000US-0174850P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-594638/56.
XX
PT Fifty nucleic acid molecules encoding human secreted proteins, useful in
PT the prevention, treatment and diagnosis of cancer, immune disorders,
PT cardiovascular disorders and neurological diseases.
XX
PS Disclosure; Page 390; 391pp; English.
XX
CC The polynucleotide sequences given in AAC74337 to AAC74386 encode the
CC human secreted proteins given in AAB39402 to AAB39451. AAB39452 to
CC AAB39484 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
CC antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
CC vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and
CC cardiant. The polynucleotides and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides
CC can also be used as a food additive or preservative to increase or
CC decrease storage capabilities. The polynucleotide are useful for
CC chromosome identification. They are also useful as probes for diagnosing
CC a disorder related to the female reproductive system, particularly breast
CC and/or ovary cancer. They are also useful in the gene therapy of breast
CC and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies,
CC agonists and antagonists are useful in the diagnosis, treatment and
CC prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular
CC disorders; (d) wound healing; (e) neurological diseases; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 54 AA;

Query Match 81.9%; Score 181; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.8e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 20 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 54

RESULT 5
ADE57598
ID ADE57598 standard; protein; 115 AA.
XX
AC ADE57598;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 3460.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 81.9%; Score 181; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 6
ADE57612
ID ADE57612 standard; protein; 115 AA.
XX
AC ADE57612;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3474.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX

OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 81.9%; Score 181; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 7
ADE60831
ID ADE60831 standard; protein; 115 AA.
XX
AC ADE60831;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 6743.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 81.9%; Score 181; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 8
ADE57606
ID ADE57606 standard; protein; 115 AA.
XX

```
AC   ADE57606;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P19065, SEQ ID NO 3468.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P19065.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 115 AA;

  Query Match             81.9%;  Score 181;  DB 7;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
```

```
RESULT 9
ADE60829
ID   ADE60829 standard; protein; 115 AA.
XX
AC   ADE60829;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Rat Protein Q64357, SEQ ID NO 6741.
XX
KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS   Rattus norvegicus.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; Q64357.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a rat protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 115 AA;

  Query Match             81.9%;  Score 181;  DB 7;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
```

RESULT 10
ADE57600
ID ADE57600 standard; protein; 115 AA.
XX
AC ADE57600;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3462.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

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  Query Match             81.9%;  Score 181;  DB 7;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93
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RESULT 11
ADE57604
ID ADE57604 standard; protein; 115 AA.
XX
AC ADE57604;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3466.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at

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CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 115 AA;

  Query Match             81.9%;  Score 181;  DB 7;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93


RESULT 12
ADE57596
ID   ADE57596 standard; protein; 115 AA.
XX
AC   ADE57596;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Rat Protein Q64357, SEQ ID NO 3458.
XX
KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS   Rattus norvegicus.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; Q64357.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a rat protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 115 AA;

  Query Match             81.9%;  Score 181;  DB 7;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93


RESULT 13
ADE57602
ID   ADE57602 standard; protein; 115 AA.
XX
AC   ADE57602;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P19065, SEQ ID NO 3464.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; P19065.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
```

CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 81.9%; Score 181; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
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Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 14
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AC ADE57610;
XX
DT 29-JAN-2004 (first entry)
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DE Human Protein P19065, SEQ ID NO 3472.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS *Homo sapiens*.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P19065.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
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CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 81.9%; Score 181; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

RESULT 15
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ID ADE57592 standard; protein; 115 AA.
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AC ADE57592;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3454.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
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CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
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CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 81.9%; Score 181; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93

Search completed: November 1, 2004, 18:04:04
Job time : 109 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 28.125 Seconds
(without alignments)
99.035 Million cell updates/sec

Title: US-10-802-574-9
Perfect score: 221
Sequence: 1 XGGLSELDDRADALQAGASQ.....TSAAKLKRKYWWKNLKGGGC 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	220	99.5	42	4	US-09-962-360B-9	Sequence 9, Appli
2	181	81.9	35	2	US-08-760-001-11	Sequence 11, Appl
3	181	81.9	35	3	US-09-015-960-11	Sequence 11, Appl
4	181	81.9	35	3	US-09-534-572-11	Sequence 11, Appl
5	181	81.9	40	4	US-09-570-022-16	Sequence 16, Appl
6	181	81.9	40	4	US-09-570-023-8	Sequence 8, Appli
7	181	81.9	116	1	US-08-409-373B-4	Sequence 4, Appli
8	181	81.9	116	1	US-08-409-373B-4	Sequence 4, Appli
9	181	81.9	116	1	US-08-393-985-16	Sequence 16, Appl
10	181	81.9	116	3	US-08-621-018B-10	Sequence 10, Appl
11	181	81.9	116	3	US-08-819-286-2	Sequence 2, Appli
12	181	81.9	116	4	US-09-483-665-10	Sequence 10, Appl
13	179	81.0	82	3	US-08-621-018B-11	Sequence 11, Appl
14	179	81.0	82	4	US-09-483-665-11	Sequence 11, Appl
15	177	80.1	35	2	US-08-760-001-9	Sequence 9, Appli
16	177	80.1	35	3	US-09-015-960-9	Sequence 9, Appli
17	177	80.1	35	3	US-09-534-572-9	Sequence 9, Appli
18	177	80.1	62	2	US-08-760-001-8	Sequence 8, Appli
19	177	80.1	62	3	US-09-015-960-8	Sequence 8, Appli
20	177	80.1	62	3	US-09-534-572-8	Sequence 8, Appli
21	176	79.6	100	3	US-08-621-018B-6	Sequence 6, Appli
22	176	79.6	100	4	US-09-483-665-6	Sequence 6, Appli
23	176	79.6	103	1	US-08-409-373B-3	Sequence 3, Appli
24	176	79.6	103	1	US-08-409-373B-3	Sequence 3, Appli
25	176	79.6	103	3	US-08-621-018B-9	Sequence 9, Appli
26	176	79.6	103	4	US-09-483-665-9	Sequence 9, Appli
27	176	79.6	347	4	US-09-513-783A-28	Sequence 28, Appl
28	176	79.6	347	4	US-09-430-656-30	Sequence 30, Appl
29	176	79.6	350	4	US-09-513-783A-30	Sequence 30, Appl
30	176	79.6	350	4	US-09-430-656-28	Sequence 28, Appl
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34	117	52.9	56	3	US-08-819-286-5	Sequence 5, Appli
35	104	47.1	94	4	US-09-621-976-6274	Sequence 6274, Ap
36	93	42.1	20	3	US-08-819-286-13	Sequence 13, Appl
37	89	40.3	71	4	US-09-621-976-5656	Sequence 5656, Ap
38	88	39.8	86	4	US-09-513-999C-5451	Sequence 5451, Ap
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41	88	39.8	102	3	US-08-621-018B-2	Sequence 2, Appli
42	88	39.8	102	4	US-09-483-665-2	Sequence 2, Appli
43	82.5	37.3	46	4	US-09-962-360B-10	Sequence 10, Appl
44	76	34.4	141	3	US-08-621-018B-8	Sequence 8, Appli
45	76	34.4	141	4	US-09-483-665-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
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; Sequence 9, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-flureseinyl-glycine
US-09-962-360B-9

Query Match 99.5%; Score 220; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKGGGC 42
||||||||||||||||||||||||||||||||||||||||||
Db 2 GGLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKGGGC 42

RESULT 2
US-08-760-001-11
; Sequence 11, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-760-001-11

Query Match 81.9%; Score 181; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35

RESULT 3
US-09-015-960-11
; Sequence 11, Application US/09015960
; Patent No. 6043042
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-015-960-11

Query Match 81.9%; Score 181; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35

RESULT 4
US-09-534-572-11
; Sequence 11, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-534-572-11

  Query Match             81.9%;  Score 181;  DB 3;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db          1 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 35


RESULT 5
US-09-570-022-16
; Sequence 16, Application US/09570022
; Patent No. 6573244
; GENERAL INFORMATION:
;  APPLICANT: GORDON, RICHARD K.
;  APPLICANT:  MOORAD, DEBORAH R.
;  APPLICANT:  DOCTOR, BHUPENDRA P.
;  APPLICANT:  GARCIA, GREGORY E.
;  TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
;  TITLE OF INVENTION:  FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
;  FILE REFERENCE: 38644-170531
;  CURRENT APPLICATION NUMBER: US/09/570,022
;  CURRENT FILING DATE:  2000-05-12
;  PRIOR APPLICATION NUMBER: 60/134,446
;  PRIOR FILING DATE: 1999-05-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-570-022-16

  Query Match             81.9%;  Score 181;  DB 4;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db          6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40


RESULT 6
US-09-570-023-8
; Sequence 8, Application US/09570023
; Patent No. 6713444
; GENERAL INFORMATION:
;  APPLICANT: GARCIA, GREGORY E.
;  APPLICANT:  GORDON, RICHARD K.
;  APPLICANT:  MOORAD, DEBBIE R.
;  APPLICANT:  DOCTOR, BHUPENDRA P.
;  TITLE OF INVENTION: BUFORIN I AS A SPECIFIC INHIBITOR AND THERAPEUTIC AGENT
;  TITLE OF INVENTION:  FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
;  FILE REFERENCE: 37833-20004.00
;  CURRENT APPLICATION NUMBER: US/09/570,023
;  CURRENT FILING DATE:  2000-05-12
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: VAMP2
US-09-570-023-8

  Query Match             81.9%;  Score 181;  DB 4;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db          6 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 40


RESULT 7
US-08-409-373B-4
; Sequence 4, Application US/08409373B
; Patent No. 5585240
;  GENERAL INFORMATION:
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  CELLUBREVIN HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/409,373B
;      FILING DATE:  23-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luther, Barbara J
;      REGISTRATION NUMBER:  33,954
;      REFERENCE/DOCKET NUMBER:  PF-0029 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-852-0195
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  116 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  X76199
US-08-409-373B-4

  Query Match             81.9%;  Score 181;  DB 1;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 8
US-08-409-373B-4
; Sequence 4, Application US/08409373B
; Patent No. 5650280
; Patent No. 5650280 5585240
;  GENERAL INFORMATION:
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  CELLUBREVIN HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
```

; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,373B
; FILING DATE: 23-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0029 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: X76199
US-08-409-373B-4

Query Match 81.9%; Score 181; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 9
US-08-393-985-16
; Sequence 16, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-16

Query Match 81.9%; Score 181; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 10
US-08-621-018B-10
; Sequence 10, Application US/08621018B
; Patent No. 6060239
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,018B
; FILING DATE: March 22, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,373
; FILING DATE: March 23, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0029-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 433075
US-08-621-018B-10

Query Match 81.9%; Score 181; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||

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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 11
US-08-819-286-2
; Sequence 2, Application US/08819286
; Patent No. 6169074
;  GENERAL INFORMATION:
;    APPLICANT:  Montal, Mauricio
;    TITLE OF INVENTION:  PEPTIDE INHIBITORS OF
;    TITLE OF INVENTION:  NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,286
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,599
;      FILING DATE:  18-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Taylor, Stacy L.
;      REGISTRATION NUMBER:  34,842
;      REFERENCE/DOCKET NUMBER:  07349/005001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  116 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-819-286-2

  Query Match             81.9%;  Score 181;  DB 3;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 12
US-09-483-665-10
; Sequence 10, Application US/09483665
; Patent No. 6534275
;  GENERAL INFORMATION:
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  CELLUBREVIN HOMOLOGS
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/483,665
;      FILING DATE:  Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,018
;      FILING DATE:  March 22, 1996
;      APPLICATION NUMBER:  08/409,373
;      FILING DATE:  March 23, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hamlet-Cox, Diana
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  PF-0029-2 DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-849-8886
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  116 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  GI 433075
US-09-483-665-10

  Query Match             81.9%;  Score 181;  DB 4;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-17;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 13
US-08-621-018B-11
; Sequence 11, Application US/08621018B
; Patent No. 6060239
;  GENERAL INFORMATION:
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  CELLUBREVIN HOMOLOGS
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,018B
;      FILING DATE:  March 22, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/409,373
;      FILING DATE:  March 23, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CERRONE, MICHAEL C.
```

```
;       REGISTRATION NUMBER:  39,132
;       REFERENCE/DOCKET NUMBER:  PF-0029-1 CIP
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-855-0555
;       TELEFAX:  650-845-4166
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  82 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GENBANK
;       CLONE:  GI 606978
US-08-621-018B-11

  Query Match             81.0%;  Score 179;  DB 3;  Length 82;
  Best Local Similarity   97.1%;  Pred. No. 9.1e-17;
  Matches   34;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              ||||||||||||||||||||||||||||||||||:|
Db         26 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 60


RESULT 14
US-09-483-665-11
; Sequence 11, Application US/09483665
; Patent No. 6534275
;  GENERAL INFORMATION:
;    APPLICANT:  Stuart, Susan G.
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    APPLICANT:  Murry, Lynn E.
;    TITLE OF INVENTION:  CELLUBREVIN HOMOLOGS
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/483,665
;      FILING DATE:  Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,018
;      FILING DATE:  March 22, 1996
;      APPLICATION NUMBER:  08/409,373
;      FILING DATE:  March 23, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hamlet-Cox, Diana
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  PF-0029-2 DIV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-849-8886
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  82 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  GI 606978
US-09-483-665-11

  Query Match             81.0%;  Score 179;  DB 4;  Length 82;
  Best Local Similarity   97.1%;  Pred. No. 9.1e-17;
  Matches   34;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
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Db         26 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 60


RESULT 15
US-08-760-001-9
; Sequence 9, Application US/08760001
; Patent No. 5962637
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford C.
;    APPLICANT:  Hallis, Bassam
;    APPLICANT:  James, Benjamin A. F.
;    APPLICANT:  Quinn, Conrad P.
;    TITLE OF INVENTION:  TOXIN ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/760,001
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB95/01279
;      FILING DATE:  02-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0120001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-760-001-9

  Query Match             80.1%;  Score 177;  DB 2;  Length 35;
  Best Local Similarity   97.1%;  Pred. No. 6.6e-17;
  Matches   34;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              ||||||||||||||||||:||||||||||||||||
Db          1 LSELDDRADALQAGASQFESSAAKLKRKYWWKNLK 35


Search completed: November  1, 2004, 18:19:42
Job time : 29.125 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 82.875 Seconds
(without alignments)
164.308 Million cell updates/sec

Title: US-10-802-574-9
Perfect score: 221
Sequence: 1 XGGLSELDDRADALQAGASQ.....TSAAKLKRKYWWKNLKGGGC 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	220	99.5	42	10	US-09-962-360B-9	Sequence 9, Appli
2	181	81.9	116	10	US-09-942-024-4	Sequence 4, Appli
3	181	81.9	116	10	US-09-942-024-17	Sequence 17, Appl
4	181	81.9	116	10	US-09-942-024-18	Sequence 18, Appl
5	181	81.9	116	10	US-09-942-098-4	Sequence 4, Appli
6	181	81.9	116	10	US-09-942-098-17	Sequence 17, Appl
7	181	81.9	116	10	US-09-942-098-18	Sequence 18, Appl
8	181	81.9	116	14	US-10-357-028-10	Sequence 10, Appl
9	181	81.9	116	15	US-10-261-161-11	Sequence 11, Appl
10	181	81.9	116	15	US-10-261-161-12	Sequence 12, Appl
11	181	81.9	116	15	US-10-261-161-13	Sequence 13, Appl
12	181	81.9	607	10	US-09-293-670-55	Sequence 55, Appl
13	179	81.0	82	14	US-10-357-028-11	Sequence 11, Appl
14	179	81.0	114	10	US-09-942-024-19	Sequence 19, Appl
15	179	81.0	114	10	US-09-942-098-19	Sequence 19, Appl
16	179	81.0	114	15	US-10-261-161-14	Sequence 14, Appl
17	176	79.6	100	14	US-10-357-028-6	Sequence 6, Appli
18	176	79.6	103	14	US-10-357-028-9	Sequence 9, Appli
19	176	79.6	347	14	US-10-100-957A-28	Sequence 28, Appl
20	176	79.6	350	14	US-10-100-957A-30	Sequence 30, Appl
21	176	79.6	365	10	US-09-293-670-52	Sequence 52, Appl
22	172	77.8	117	16	US-10-467-595-27	Sequence 27, Appl
23	172	77.8	118	10	US-09-942-024-96	Sequence 96, Appl
24	172	77.8	118	10	US-09-942-098-96	Sequence 96, Appl
25	172	77.8	118	15	US-10-261-161-10	Sequence 10, Appl
26	170	76.9	35	10	US-09-962-360B-4	Sequence 4, Appli
27	169	76.5	35	10	US-09-962-360B-3	Sequence 3, Appli
28	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl
29	161	72.9	40	10	US-09-942-024-60	Sequence 60, Appl
30	161	72.9	40	10	US-09-942-024-61	Sequence 61, Appl
31	161	72.9	40	10	US-09-942-098-58	Sequence 58, Appl
32	161	72.9	40	10	US-09-942-098-60	Sequence 60, Appl
33	161	72.9	40	10	US-09-942-098-61	Sequence 61, Appl
34	161	72.9	40	15	US-10-261-161-83	Sequence 83, Appl
35	161	72.9	40	15	US-10-261-161-85	Sequence 85, Appl
36	161	72.9	40	15	US-10-261-161-86	Sequence 86, Appl
37	159	71.9	109	14	US-10-369-493-6364	Sequence 6364, Ap
38	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl
39	157	71.0	40	10	US-09-942-024-65	Sequence 65, Appl
40	157	71.0	40	10	US-09-942-098-57	Sequence 57, Appl
41	157	71.0	40	10	US-09-942-098-65	Sequence 65, Appl
42	157	71.0	40	15	US-10-261-161-82	Sequence 82, Appl
43	157	71.0	40	15	US-10-261-161-90	Sequence 90, Appl
44	157	71.0	104	10	US-09-942-024-20	Sequence 20, Appl
45	157	71.0	104	10	US-09-942-098-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-fluresceinyl-glycine
US-09-962-360B-9

Query Match 99.5%; Score 220; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-22;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKGGGC 42
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Db 2 GGLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKGGGC 42

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RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Botulinum
;  TITLE OF INVENTION:  Serotype A/E Toxins
;  FILE REFERENCE: P-AR 4803
;  CURRENT APPLICATION NUMBER: US/09/942,024
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-942-024-4

  Query Match             81.9%;  Score 181;  DB 10;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Botulinum
;  TITLE OF INVENTION:  Serotype A/E Toxins
;  FILE REFERENCE: P-AR 4803
;  CURRENT APPLICATION NUMBER: US/09/942,024
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-942-024-17

  Query Match             81.9%;  Score 181;  DB 10;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Botulinum
;  TITLE OF INVENTION:  Serotype A/E Toxins
;  FILE REFERENCE: P-AR 4803
;  CURRENT APPLICATION NUMBER: US/09/942,024
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-942-024-18

  Query Match             81.9%;  Score 181;  DB 10;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Clostridial
;  TITLE OF INVENTION:  Toxins
;  FILE REFERENCE: P-AR 4802
;  CURRENT APPLICATION NUMBER: US/09/942,098
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-942-098-4

  Query Match             81.9%;  Score 181;  DB 10;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Clostridial
;  TITLE OF INVENTION:  Toxins
;  FILE REFERENCE: P-AR 4802
;  CURRENT APPLICATION NUMBER: US/09/942,098
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-942-098-17

  Query Match             81.9%;  Score 181;  DB 10;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 7
US-09-942-098-18
; Sequence 18, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
;  APPLICANT: Steward, Lance E.
;  APPLICANT:  Fernandez-Salas, Ester
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Fret Protease Assays For Clostridial
;  TITLE OF INVENTION:  Toxins
;  FILE REFERENCE: P-AR 4802
;  CURRENT APPLICATION NUMBER: US/09/942,098
;  CURRENT FILING DATE:  2001-08-28
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-942-098-18

  Query Match             81.9%;  Score 181;  DB 10;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
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Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 8
US-10-357-028-10
; Sequence 10, Application US/10357028
; Publication No. US20030180931A1
;   GENERAL INFORMATION:
;        APPLICANT: Stuart, Susan G.
;                   Hawkins, Phillip R.
;                   Seilhamer, Jeffrey J.
;                   Murry, Lynn E.
;        TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
;        NUMBER OF SEQUENCES: 51
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Incyte Pharmaceuticals, Inc.
;             STREET: 3174 Porter Drive
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: U.S.
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 1.5
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/357,028
;             FILING DATE: 29-Jan-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/483,665
;             FILING DATE: Herewith
;             APPLICATION NUMBER: 08/621,018
;             FILING DATE: March 22, 1996
;             APPLICATION NUMBER: 08/409,373
;             FILING DATE: March 23, 1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hamlet-Cox, Diana
;             REGISTRATION NUMBER: 33,302
;             REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-855-0555
;             TELEFAX: 650-849-8886
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 116 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        IMMEDIATE SOURCE:
;             LIBRARY: GENBANK
;             CLONE: GI 433075
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-357-028-10

  Query Match             81.9%;  Score 181;  DB 14;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 9
US-10-261-161-11
; Sequence 11, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
;  APPLICANT: Fernandez-Salas, Ester
;  APPLICANT:  Steward, Lance E.
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
;  TITLE OF INVENTION:  Transfer (FRET) Assays For Clostridial Toxins
;  FILE REFERENCE: P-AR 4804
;  CURRENT APPLICATION NUMBER: US/10/261,161
;  CURRENT FILING DATE:  2002-09-27
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-261-161-11

  Query Match             81.9%;  Score 181;  DB 15;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 4e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 10
US-10-261-161-12
; Sequence 12, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
;  APPLICANT: Fernandez-Salas, Ester
;  APPLICANT:  Steward, Lance E.
;  APPLICANT:  Aoki, Kei Roger
;  TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
;  TITLE OF INVENTION:  Transfer (FRET) Assays For Clostridial Toxins
;  FILE REFERENCE: P-AR 4804
;  CURRENT APPLICATION NUMBER: US/10/261,161
;  CURRENT FILING DATE:  2002-09-27
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 116
;   TYPE: PRT
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; ORGANISM: Mus musculus
US-10-261-161-12

Query Match 81.9%; Score 181; DB 15; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 11
US-10-261-161-13
; Sequence 13, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-261-161-13

Query Match 81.9%; Score 181; DB 15; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94

RESULT 12
US-09-293-670-55
; Sequence 55, Application US/09293670
; Publication No. US20030190684A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Joseph
; APPLICANT: Lorens, James
; APPLICANT: Payan, Donald
; APPLICANT: Rossi, Alexander
; TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in
; TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule
; TITLE OF INVENTION: Libraries
; FILE REFERENCE: A68104/DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/293,670
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-293-670-55

Query Match 81.9%; Score 181; DB 10; Length 607;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||||
Db 61 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 95

RESULT 13
US-10-357-028-11
; Sequence 11, Application US/10357028
; Publication No. US20030180931A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; Hawkins, Phillip R.
; Seilhamer, Jeffrey J.
; Murry, Lynn E.
; TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/357,028
; FILING DATE: 29-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/483,665
; FILING DATE: Herewith
; APPLICATION NUMBER: 08/621,018
; FILING DATE: March 22, 1996
; APPLICATION NUMBER: 08/409,373
; FILING DATE: March 23, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-Cox, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-849-8886
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 606978
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-357-028-11

Query Match 81.0%; Score 179; DB 14; Length 82;
Best Local Similarity 97.1%; Pred. No. 5.1e-16;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||:|
Db 26 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 60

RESULT 14
US-09-942-024-19
; Sequence 19, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-942-024-19

Query Match 81.0%; Score 179; DB 10; Length 114;
Best Local Similarity 97.1%; Pred. No. 7.2e-16;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||:|
Db 58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 92

RESULT 15
US-09-942-098-19
; Sequence 19, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-942-098-19

Query Match 81.0%; Score 179; DB 10; Length 114;
Best Local Similarity 97.1%; Pred. No. 7.2e-16;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||||||||||||||||:|
Db 58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 92

Search completed: November 1, 2004, 18:23:48
Job time : 83.875 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 ; Search time 21.75 Seconds
(without alignments)
185.798 Million cell updates/sec

Title: US-10-802-574-9
Perfect score: 221
Sequence: 1 XGGLSELDDRADALQAGASQ.....TSAAKLKRKYWWKNLKGGGC 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	181	81.9	116	2	B38315	synaptobrevin 2 -
2	181	81.9	116	2	JN0011	synaptobrevin 2 -
3	181	81.9	116	2	B34288	synaptobrevin 2 -
4	176	79.6	103	2	S35077	cellubrevin - rat
5	172	77.8	118	2	S52747	Vampl protein - hu
6	172	77.8	118	2	A38315	synaptobrevin 1 -
7	172	77.8	120	2	A32146	vesicle-associated
8	165	74.7	118	2	A34288	vesicle-associated
9	161	72.9	125	2	S40153	synaptobrevin - lo
10	159	71.9	109	2	T33239	synaptobrevin SNB-
11	127	57.5	32	2	S35555	vesicle-associated
12	127	57.5	32	2	S35554	vesicle-associated
13	123	55.7	32	2	S35552	vesicle-associated
14	119	53.8	132	2	JC1522	synaptobrevin isof
15	119	53.8	152	2	JC1521	synaptobrevin isof
16	116	52.5	32	2	S35553	vesicle-associated
17	113	51.1	145	2	T21318	hypothetical prote
18	92	41.6	223	2	S47654	integral membrane
19	82	37.1	115	2	S62059	synaptobrevin homo
20	75	33.9	121	2	T39073	synaptobrevin homo
21	72	32.6	117	2	S31250	synaptobrevin homo
22	72	32.6	220	2	T00801	probable synaptobr
23	70	31.7	1237	1	GNFF42	HIV-1 retropepsin
24	68	30.8	60	2	D44088	homeotic protein H
25	68	30.8	221	2	F84741	probable synaptobr
26	66	29.9	175	2	D86180	hypothetical prote
27	64	29.0	251	2	AD1145	cyclase HisF homol
28	62.5	28.3	515	2	S59811	vacuolar segregati
29	62	28.1	229	2	F86180	hypothetical prote
30	62	28.1	251	2	AD1504	cyclase HisF homol
31	59	26.7	251	2	S64927	probable membrane
32	59	26.7	609	2	AB0500	glutamine-fructose
33	58	26.2	102	2	S44781	C30A5.4 protein -
34	58	26.2	102	2	T24909	hypothetical prote
35	58	26.2	450	2	A97740	hypothetical prote
36	58	26.2	450	2	A71678	probable response
37	57	25.8	210	2	T16595	hypothetical prote
38	57	25.8	226	2	A97774	petR protein [impo
39	56.5	25.6	588	2	G82118	succinate dehydrog
40	56	25.3	219	2	T04630	synaptobrevin homo
41	56	25.3	240	2	T47589	synaptobrevin-like
42	56	25.3	454	2	AI1641	anthranilate synth
43	56	25.3	663	2	H82731	glutaryl-7-ACA acy
44	55	24.9	565	2	S10367	carboxylesterase (
45	55	24.9	788	2	T44262	transducer protein

ALIGNMENTS

RESULT 1
B38315
synaptobrevin 2 - human
C;Species: Homo sapiens (man)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C;Accession: B38315
R;Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A;Title: Structures and chromosomal localizations of two human genes encoding synaptobrev
A;Reference number: A38315; MUID:91009161; PMID:1976629
A;Accession: B38315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-116 <ARC>
A;Cross-references: UNIPROT:P19065; GB:M36205; GB:J05611; NID:g338630; PIDN:AAA60604.1;
C;Genetics:
A;Gene: GDB:SYB2; VAMP-2
A;Cross-references: GDB:125293; OMIM:185881
A;Map position: 17pter-17p12
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

Query Match 81.9%; Score 181; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94
```

RESULT 2
JN0011
synaptobrevin 2 - bovine
N;Alternate names: SNAP receptor
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: JN0011; S36811; S32363
R;Suedhof, T.C.; Baumert, M.; Perin, M.S.; Jahn, R.
Neuron 2, 1475-1481, 1989
A;Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.
A;Reference number: A93413; MUID:90180466; PMID:2560644
A;Accession: JN0011
A;Molecule type: mRNA
A;Residues: 1-116 <SUE>
A;Cross-references: UNIPROT:P19065; GB:X76199; NID:g433075; PIDN:CAA53792.1; PID:g433076
A;Experimental source: brain
R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A;Reference number: S36811; MUID:93374072; PMID:8365494
A;Accession: S36811

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A;Molecule type: mRNA
A;Residues: 'X',48-79 <HOR>
A;Experimental source: brain
R;Soellner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Geromanos, S.; Tem
Nature 362, 318-324, 1993
A;Title: SNAP receptors implicated in vesicle targeting and fusion.
A;Reference number: S32360; MUID:93205116; PMID:8455717
A;Accession: S32363
A;Molecule type: protein
A;Residues: 31-47,'X',49-55,'X',57-59;67-82 <SOE>
A;Experimental source: brain
C;Comment: This protein is an intrinsic membrane protein of small synaptic vesicles.
C;Superfamily: synaptobrevin
C;Keywords: acetylated amino end; membrane trafficking; transmembrane protein
F;2-116/Product: synaptobrevin 2 #status predicted <MAT>
F;95-114/Domain: transmembrane #status predicted <TMM>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

  Query Match             81.9%;  Score 181;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 3
B34288
synaptobrevin 2 - rat
N;Alternate names: vesicle-associated membrane protein 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
C;Accession: B34288; S27125
R;Elferink, L.A.; Trimble, W.S.; Scheller, R.H.
J. Biol. Chem. 264, 11061-11064, 1989
A;Title: Two vesicle-associated membrane protein genes are differentially expressed in t
A;Reference number: A34288; MUID:89291844; PMID:2472388
A;Accession: B34288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <ELF>
A;Cross-references: UNIPROT:Q64357; GB:M24105; GB:J04827; NID:g207626; PIDN:AAA42321.1;
R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R
Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt
A;Reference number: S27125; MUID:93063293; PMID:1331807
A;Accession: S27125
A;Molecule type: protein
A;Residues: 77-99,'X',101 <SCH>
C;Superfamily: synaptobrevin
C;Keywords: membrane protein; membrane trafficking; synaptic vesicle

  Query Match             81.9%;  Score 181;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 4
S35077
cellubrevin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S35077
R;McMahon, H.T.; Ushkaryov, Y.A.; Edelmann, L.; Link, E.; Binz, T.; Niemann, H.; Jahn, R
Nature 364, 346-349, 1993
A;Title: Cellubrevin is a ubiquitous tetanus-toxin substrate homologous to a putative sy
A;Reference number: S35077; MUID:93323976; PMID:8332193
A;Accession: S35077
A;Molecule type: mRNA
A;Residues: 1-103 <MCM>
A;Cross-references: UNIPROT:Q64271; GB:S63830; NID:g388482; PIDN:AAB27554.1; PID:g388483
C;Superfamily: synaptobrevin

  Query Match             79.6%;  Score 176;  DB 2;  Length 103;
  Best Local Similarity   97.1%;  Pred. No. 7.6e-16;
  Matches   34;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||| |
Db         47 LSELDDRADALQAGASQFETSAAKLKRKYWWKNCK 81


RESULT 5
S52747
Vamp1 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52747
R;Gough, K.H.; Verkuylen, A.; Cosgrove, L.; Frenkel, M.J.; Ward, C.W.
submitted to the EMBL Data Library, December 1994
A;Description: Isolation and sequence analysis of SNAREs from human skeletal muscle.
A;Reference number: S52747
A;Accession: S52747
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <GOU>
A;Cross-references: UNIPROT:P23763; EMBL:Z48924; NID:g758107; PIDN:CAA88760.1; PID:g7581(
C;Superfamily: synaptobrevin

  Query Match             77.8%;  Score 172;  DB 2;  Length 118;
  Best Local Similarity   94.3%;  Pred. No. 2.9e-15;
  Matches   33;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||:|||||||||||||| |
Db         62 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 96


RESULT 6
A38315
synaptobrevin 1 - human
C;Species: Homo sapiens (man)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C;Accession: A38315
R;Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A;Title: Structures and chromosomal localizations of two human genes encoding synaptobrev
A;Reference number: A38315; MUID:91009161; PMID:1976629
A;Accession: A38315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <ARC>
A;Cross-references: UNIPROT:P23763; GB:M36200; GB:J05611; NID:g338623; PIDN:AAA60603.1; P
C;Genetics:
A;Gene: GDB:SYB1; VAMP-1
A;Cross-references: GDB:125292; OMIM:185880
A;Map position: 12p-12p
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

  Query Match             77.8%;  Score 172;  DB 2;  Length 118;
  Best Local Similarity   94.3%;  Pred. No. 2.9e-15;
  Matches   33;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||:|||||||||||||| |
Db         62 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 96


RESULT 7
A32146
```

vesicle-associated membrane protein 1 - Pacific electric ray
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C;Accession: A32146
R;Trimble, W.S.; Cowan, D.M.; Scheller, R.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 4538-4542, 1988
A;Title: VAMP-1: a synaptic vesicle-associated integral membrane protein.
A;Reference number: A32146; MUID:88248054; PMID:3380805
A;Accession: A32146
A;Molecule type: mRNA
A;Residues: 1-120 <TRI>
A;Cross-references: UNIPROT:P13701; EMBL:J03777; NID:g213245; PIDN:AAA49286.1; PID:g2132
C;Superfamily: synaptobrevin
C;Keywords: membrane protein

Query Match 77.8%; Score 172; DB 2; Length 120;
Best Local Similarity 94.3%; Pred. No. 3e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||||||||||||||||||||:||||||||||||| |
Db 64 LSELDDRADALQAGASQFESSAAKLKRKYWWKNCK 98

RESULT 8
A34288
vesicle-associated membrane protein 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34288
R;Elferink, L.A.; Trimble, W.S.; Scheller, R.H.
J. Biol. Chem. 264, 11061-11064, 1989
A;Title: Two vesicle-associated membrane protein genes are differentially expressed in t
A;Reference number: A34288; MUID:89291844; PMID:2472388
A;Accession: A34288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <ELF>
A;Cross-references: UNIPROT:Q63666; GB:M24104; GB:J04827; NID:g207628; PIDN:AAA42322.1;
C;Superfamily: synaptobrevin
C;Keywords: membrane protein

Query Match 74.7%; Score 165; DB 2; Length 118;
Best Local Similarity 91.4%; Pred. No. 2.4e-14;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
|||||||||||||||| ||:||||||||||||| |
Db 62 LSELDDRADALQAGASVFESSAAKLKRKYWWKNCK 96

RESULT 9
S40153
synaptobrevin - longfin squid
C;Species: Loligo pealeii (longfin squid)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40153
R;Bommert, K.; Kistner, A.; Hasermann, E.; Betz, H.
submitted to the EMBL Data Library, August 1993
A;Description: Conservation of primary structure and clostridial neurotoxin cleavage sit
A;Reference number: S40153
A;Accession: S40153
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <BOM>
A;Cross-references: UNIPROT:P47194; EMBL:X74748; NID:g437855; PIDN:CAA52766.1; PID:g4378
C;Superfamily: synaptobrevin

Query Match 72.9%; Score 161; DB 2; Length 125;
Best Local Similarity 85.7%; Pred. No. 8.6e-14;
Matches 30; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
:|||||||||||||||||| || |||||:|||| |
Db 69 ISELDDRADALQAGASQFEASAGKLKRKFWWKNCK 103

RESULT 10
T33239
synaptobrevin SNB-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33239
R;Greco, T.; Bradshaw, H.; O'Brien, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T10H9.
A;Reference number: Z21306
A;Accession: T33239
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-109 <GRE>
A;Cross-references: UNIPROT:O02495; EMBL:AF067949; PIDN:AAC19234.1; GSPDB:GN00023; CESP:T
A;Experimental source: strain Bristol N2; clone T10H9
C;Genetics:
A;Gene: SNB-1; CESP:T10H9.4
A;Map position: 5
A;Introns: 39/3
C;Superfamily: synaptobrevin

Query Match 71.9%; Score 159; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.4e-13;
Matches 30; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
||:|||||||| |||||| ||| |||||||||:|
Db 52 LSQLDDRADALQEGASQFEKSAATLKRKYWWKNIK 86

RESULT 11
S35555
vesicle-associated membrane protein 2 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S35555
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35555
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q7LZ64
C;Superfamily: synaptobrevin
C;Keywords: membrane trafficking; transmembrane protein

Query Match 57.5%; Score 127; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAAKLKR 30
|||||||||||||||||||||||||||
Db 6 LSELDDRADALQAGASQFETSAAKLKR 32

RESULT 12
S35554
vesicle-associated membrane protein 2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S35554
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35554
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:O35619
C;Superfamily: synaptobrevin

Query Match 57.5%; Score 127; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 LSELDDRADALQAGASQFETSAAKLKR 30
              |||||||||||||||||||||||||||
Db          6 LSELDDRADALQAGASQFETSAAKLKR 32
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RESULT 13
S35552
vesicle-associated membrane protein 1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S35552
R;Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35552
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q9CXX2
C;Superfamily: synaptobrevin

Query Match 55.7%; Score 123; DB 2; Length 32;
Best Local Similarity 96.3%; Pred. No. 1.9e-09;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 LSELDDRADALQAGASQFETSAAKLKR 30
              |||||||||||||||||||:|||||||
Db          6 LSELDDRADALQAGASQFESSAAKLKR 32
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RESULT 14
JC1522
synaptobrevin isoform B - fruit fly (Drosophila melanogaster)
N;Alternate names: vesicle-associated membrane protein B
C;Species: Drosophila melanogaster
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: JC1522
R;Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.
Gene 131, 175-181, 1993
A;Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene
A;Reference number: JC1521; MUID:94010306; PMID:8406010
A;Accession: JC1522
A;Molecule type: DNA
A;Residues: 1-132 <CHI>
A;Cross-references: UNIPROT:P18489; GB:L14270; NID:g290281; PIDN:AAA28923.1; PID:g290282
A;Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue
C;Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobre
C;Genetics:
A;Gene: syb
A;Cross-references: FlyBase:FBgn0003660
A;Introns: 16/2; 128/1
C;Superfamily: synaptobrevin
C;Keywords: membrane protein; synaptic vesicle

Query Match 53.8%; Score 119; DB 2; Length 132;
Best Local Similarity 65.7%; Pred. No. 2.8e-08;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

```
Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||| :||| |: |||| |  | ||||| || |:|
Db         76 LSELGERADQLEQGASQSEQQAGKLKRKQWWANMK 110
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RESULT 15
JC1521
synaptobrevin isoform A - fruit fly (Drosophila melanogaster)
N;Alternate names: vesicle-associated membrane protein A
C;Species: Drosophila melanogaster
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: JC1521; JN0012
R;Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.
Gene 131, 175-181, 1993
A;Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene
A;Reference number: JC1521; MUID:94010306; PMID:8406010
A;Accession: JC1521
A;Molecule type: DNA
A;Residues: 1-152 <CHI>
A;Cross-references: UNIPROT:P18489; GB:L14270; NID:g290281; PIDN:AAA28924.1; PID:g290283
A;Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue
R;Suedhof, T.C.; Baumert, M.; Perin, M.S.; Jahn, R.
Neuron 2, 1475-1481, 1989
A;Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.
A;Reference number: A93413; MUID:90180466; PMID:2560644
A;Accession: JN0012
A;Molecule type: mRNA
A;Residues: 1-92,'F',94-152 <SUE>
C;Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobrev
C;Genetics:
A;Gene: syb
A;Cross-references: FlyBase:FBgn0003660
A;Introns: 16/2; 128/1
C;Superfamily: synaptobrevin
C;Keywords: synaptic vesicle; transmembrane protein
F;111-130/Domain: transmembrane #status predicted <TMM>

Query Match 53.8%; Score 119; DB 2; Length 152;
Best Local Similarity 65.7%; Pred. No. 3.3e-08;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

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Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||| :||| |: |||| |  | ||||| || |:|
Db         76 LSELGERADQLEQGASQSEQQAGKLKRKQWWANMK 110
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Search completed: November 1, 2004, 17:53:52
Job time : 21.75 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 116.625 Seconds
(without alignments)
207.209 Million cell updates/sec

Title: US-10-802-574-9
Perfect score: 221
Sequence: 1 XGGLSELDDRADALQAGASQ.....TSAAKLKRKYWWKNLKGGGC 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	181	81.9	81	2	Q8HZX7	Q8hzx7 oryctolagus
2	181	81.9	114	2	Q6P835	Q6p835 xenopus tro
3	181	81.9	114	2	AAH61396	Aah61396 xenopus t
4	181	81.9	115	1	VAM2_HUMAN	P19065 homo sapien
5	181	81.9	115	1	VAM2_MOUSE	Q64357 mus musculu
6	181	81.9	116	2	Q9BUC2	Q9buc2 homo sapien
7	181	81.9	116	2	Q9N0Y0	Q9n0y0 macaca mula
8	181	81.9	116	2	O35619	O35619 mus musculu
9	181	81.9	116	2	AAH02737	Aah02737 homo sapi
10	181	81.9	116	2	AAH55105	Aah55105 mus muscu
11	181	81.9	116	2	BAC41125	Bac41125 mus muscu
12	181	81.9	135	2	Q9WUW2	Q9wuw2 rattus norv
13	181	81.9	142	2	Q8CHR4	Q8chr4 mus musculu
14	179	81.0	113	1	VAM2_XENLA	P47193 xenopus lae
15	179	81.0	114	2	AAH60344	Aah60344 xenopus l
16	176	79.6	99	1	VAM3_HUMAN	Q15836 homo sapien
17	176	79.6	103	1	VAM3_MOUSE	Q64271 mus musculu
18	176	79.6	103	2	AAG42468	Aag42468 mus muscu
19	176	79.6	103	2	AAH60045	Aah60045 mus muscu
20	176	79.6	103	2	BAC34586	Bac34586 mus muscu
21	176	79.6	103	2	BAC34723	Bac34723 mus muscu
22	175	79.2	114	2	O57345	O57345 xenopus lae
23	174	78.7	102	2	Q6IQK3	Q6iqk3 brachydanio
24	174	78.7	102	2	AAH71402	Aah71402 brachydan
25	172	77.8	100	2	Q9BRV4	Q9brv4 homo sapien
26	172	77.8	117	2	Q8IVC9	Q8ivc9 homo sapien
27	172	77.8	117	2	Q6PFF3	Q6pff3 mus musculu
28	172	77.8	117	2	AAH57587	Aah57587 mus muscu
29	172	77.8	118	1	VAM1_HUMAN	P23763 homo sapien
30	172	77.8	118	1	VAM1_MOUSE	Q62442 mus musculu
31	172	77.8	118	2	BAC37151	Bac37151 mus muscu
32	172	77.8	120	1	SYB_TORCA	P13701 torpedo cal
33	172	77.8	182	2	Q9CXX2	Q9cxx2 mus musculu
34	171	77.4	110	2	Q7SZZ5	Q7szz5 brachydanio
35	171	77.4	110	2	AAH59626	Aah59626 brachydan
36	171	77.4	112	2	O57432	O57432 fugu rubrip
37	170	76.9	119	2	Q6PBJ3	Q6pbj3 brachydanio
38	170	76.9	119	2	AAH59687	Aah59687 brachydan
39	167	75.6	86	2	Q6DLT0	Q6dlt0 lateolabrax
40	167	75.6	110	2	Q8T897	Q8t897 halocynthia
41	165	74.7	116	2	Q8CH14	Q8ch14 rattus norv
42	165	74.7	117	2	O09025	O09025 rattus norv
43	165	74.7	118	1	VAM1_RAT	Q63666 rattus norv
44	162	73.3	118	2	Q6DGI1	Q6dgi1 brachydanio
45	162	73.3	160	2	Q86FE0	Q86fe0 schistosoma

ALIGNMENTS

RESULT 1
Q8HZX7
ID Q8HZX7 PRELIMINARY; PRT; 81 AA.
AC Q8HZX7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptobrevin-2 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal collecting duct;
RX PubMed=12186952;
RA Gouraud S., Laera A., Calamita G., Carmosino M., Procino G.,
RA Rossetto O., Mannucci R., Rosenthal W., Svelto M., Valenti G.;
RT "Functional involvement of VAMP/synaptobrevin-2 in cAMP-stimulated
RT aquaporin 2 translocation in renal collecting duct cells.";
RL J. Cell Sci. 115:3667-3674(2002).
DR EMBL; AF262953; AAN14408.1; -.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin; 1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; Synaptobrevin; 1.
DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR PROSITE; PS50892; V_SNARE; 1.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9357 MW; 6F171CA14775860C CRC64;

Query Match 81.9%; Score 181; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 5.3e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         32 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 66
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RESULT 2
Q6P835
ID Q6P835 PRELIMINARY; PRT; 114 AA.
AC Q6P835;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75977.
GN Name=MGC75977;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.

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OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061396; AAH61396.1; -.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   114 AA;  12440 MW;  0EE3EADBDF2A1ABE CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 92


RESULT 3
AAH61396
ID   AAH61396    PRELIMINARY;      PRT;   114 AA.
AC   AAH61396;
DT   25-MAR-2004 (TrEMBLrel. 27, Created)
DT   25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC75977.
GN   MGC75977.
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061396; AAH61396.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   114 AA;  12440 MW;  0EE3EADBDF2A1ABE CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 92


RESULT 4
VAM2_HUMAN
ID   VAM2_HUMAN     STANDARD;      PRT;   115 AA.
AC   P19065;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).
GN   Name=VAMP2; Synonyms=SYB2;
OS   Homo sapiens (Human), and
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606, 9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human;
RX   MEDLINE=91009161; PubMed=1976629;
RA   Archer B.T. III, Oezcelik T., Jahn R., Francke U., Suedhof T.C.;
RT   "Structures and chromosomal localizations of two human genes encoding
RT   synaptobrevins 1 and 2.";
RL   J. Biol. Chem. 265:17267-17273(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human; TISSUE=Peripheral blood;
RA   Nabokina S.M., Lazo P.A., Mollinedo F.;
RT   "Expression of VAMP genes in human neutrophils.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human; TISSUE=Blood;
RA   Taruscio D., Zoraqi K.G., Falbo V.;
RT   "Genomic structure of human SYB2 gene.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Bovine;
RX   MEDLINE=90180466; PubMed=2560644;
RA   Suedhof T.C., Baumert M., Perin M.S., Jahn R.;
RT   "A synaptic vesicle membrane protein is conserved from mammals to
RT   Drosophila.";
```

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RL   Neuron 2:1475-1481(1989).
RN   [5]
RP   SEQUENCE OF 31-59 AND 67-82, AND ACETYLATION.
RC   SPECIES=Bovine;
RX   MEDLINE=93205116; PubMed=8455717;
RA   Soellner T., Whiteheart S.W., Brunner M., Erdjument-Bromage H.,
RA   Geromanos S., Tempst P., Rothman J.E.;
RT   "SNAP receptors implicated in vesicle targeting and fusion.";
RL   Nature 362:318-324(1993).
RN   [6]
RP   TISSUE SPECIFICITY.
RC   SPECIES=Human;
RX   MEDLINE=96332494; PubMed=8760387;
RA   Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
RA   Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
RA   Ward C.W.;
RT   "Insulin-responsive tissues contain the core complex protein SNAP-25
RT   (synaptosomal-associated protein 25) A and B isoforms in addition to
RT   syntaxin 4 and synaptobrevins 1 and 2.";
RL   Biochem. J. 317:945-954(1996).
RN   [7]
RP   TOPOLOGY.
RC   SPECIES=Human;
RX   MEDLINE=95137000; PubMed=7835332;
RA   Kutay U., Ahnert-Hilger G., Hartmann E., Wiedenmann B., Rapoport T.A.;
RT   "Transport route for synaptobrevin via a novel pathway of insertion
RT   into the endoplasmic reticulum membrane.";
RL   EMBO J. 14:217-223(1995).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-88 IN COMPLEX WITH BOTB.
RC   SPECIES=Human;
RX   MEDLINE=20392548; PubMed=10932255; DOI=10.1038/77997;
RA   Hanson M.A., Stevens R.C.;
RT   "Cocrystal structure of synaptobrevin-II bound to botulinum neurotoxin
RT   type B at 2.0 A resolution.";
RL   Nat. Struct. Biol. 7:687-692(2000).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBUNIT: Interacts with VAPA and VAPB.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- TISSUE SPECIFICITY: Nervous system and skeletal muscle.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M36205; AAA60604.1; -.
DR   EMBL; M36201; AAA60604.1; JOINED.
DR   EMBL; M36202; AAA60604.1; JOINED.
DR   EMBL; M36203; AAA60604.1; JOINED.
DR   EMBL; M36204; AAA60604.1; JOINED.
DR   EMBL; AJ225044; CAA12385.1; -.
DR   EMBL; AF135372; AAF15551.1; -.
DR   EMBL; X76199; CAA53792.1; -.
DR   PIR; B38315; B38315.
DR   PIR; JN0011; JN0011.
DR   PDB; 1F83; X-ray; B=52-75, C=76-87.
DR   Genew; HGNC:12643; VAMP2.
DR   MIM; 185881; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   3D-structure; Acetylation; Coiled coil; Direct protein sequencing;
KW   Multigene family; Synapse; Synaptosome; Transmembrane.
FT   INIT_MET      0      0
FT   DOMAIN        1     93       Cytoplasmic (Potential).
FT   TRANSMEM     94    113       Anchor for type IV membrane protein
FT                                 (Potential).
FT   DOMAIN      114    115       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine.
FT   DOMAIN       30     90       v-SNARE coiled-coil homology.
SQ   SEQUENCE   115 AA;  12517 MW;  388B79F0D21AD81E CRC64;

  Query Match             81.9%;  Score 181;  DB 1;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93


RESULT 5
VAM2_MOUSE
ID   VAM2_MOUSE     STANDARD;      PRT;   115 AA.
AC   Q64357;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).
GN   Name=Vamp2; Synonyms=Syb2;
OS   Mus musculus (Mouse), and
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090, 10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Rat;
RX   MEDLINE=89291844; PubMed=2472388;
RA   Elferink L.A., Trimble W.S., Scheller R.H.;
RT   "Two vesicle-associated membrane protein genes are differentially
RT   expressed in the rat central nervous system.";
RL   J. Biol. Chem. 264:11061-11064(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Mouse;
RX   MEDLINE=98104125; PubMed=9430681;
RA   Martin L.B., Shewan A., Millar C.A., Gould G.W., James D.E.;
RT   "Vesicle-associated membrane protein 2 plays a specific role in the
RT   insulin-dependent trafficking of the facilitative glucose transporter
RT   GLUT4 in 3T3-L1 adipocytes.";
RL   J. Biol. Chem. 273:1444-1452(1998).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-96 IN COMPLEX WITH STX1A
RP   AND SNAP25.
RC   SPECIES=Rat;
RX   MEDLINE=98430524; PubMed=9759724; DOI=10.1038/26412;
RA   Sutton R.B., Fasshauer D., Jahn R., Brunger A.T.;
RT   "Crystal structure of a SNARE complex involved in synaptic exocytosis
RT   at 2.4 A resolution.";
RL   Nature 395:347-353(1998).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 29-93 IN COMPLEX WITH STX1A;
RP   CPLX1 AND SNAP25, AND NMR ANALYSIS.
RC   SPECIES=Rat;
RX   MEDLINE=21822661; PubMed=11832227;
RA   Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
RA   Suedhof T.C., Rizo J.;
RT   "Three-dimensional structure of the complexin/SNARE complex.";
RL   Neuron 33:397-409(2002).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 28-89 IN COMPLEX WITH STX1A
RP   AND SNAP25.
RC   SPECIES=Rat;
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RX   MEDLINE=22499607; PubMed=12496247; DOI=10.1074/jbc.M211889200;
RA   Ernst J.A., Brunger A.T.;
RT   "High resolution structure, stability, and synaptotagmin binding of a
RT   truncated neuronal SNARE complex.";
RL   J. Biol. Chem. 278:8630-8636(2003).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBUNIT: Interacts with VAPA and VAPB (By similarity). Part of the
CC       SNARE core complex containing SNAP25, VAMP2 and STX1A. This
CC       complex binds to CPLX1.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- TISSUE SPECIFICITY: Nervous system specific. A higher level
CC       expression is seen in the brain as compared to the spinal cord.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M24105; AAA42321.1; -.
DR   EMBL; U60150; AAB03463.1; -.
DR   PIR; B34288; B34288.
DR   PDB; 1KIL; X-ray; A=26-91.
DR   PDB; 1N7S; X-ray; A=26-88.
DR   PDB; 1SFC; X-ray; A/E/I=1-95.
DR   MGD; MGI:1313277; Vamp2.
DR   RGD; 3949; Vamp2.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   3D-structure; Acetylation; Coiled coil; Multigene family;
KW   Polymorphism; Synapse; Synaptosome; Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     93       Cytoplasmic (Potential).
FT   TRANSMEM     94    113       Anchor for type IV membrane protein
FT                                (Potential).
FT   DOMAIN      114    115       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine (By similarity).
FT   DOMAIN       30     90       v-SNARE coiled-coil homology.
FT   VARIANT     110    110       I -> II.
FT   VARIANT     111    111       V -> I.
FT   HELIX        28     87
SQ   SEQUENCE   115 AA;  12559 MW;  EA400D6291ABF0BC CRC64;

  Query Match             81.9%;  Score 181;  DB 1;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         59 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 93


RESULT 6
Q9BUC2
ID   Q9BUC2      PRELIMINARY;      PRT;   116 AA.
AC   Q9BUC2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Vesicle-associated membrane protein 2 (Synaptobrevin 2).
GN   Name=VAMP2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, Lung, and Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002737; AAH02737.3; -.
DR   EMBL; BC019608; AAH19608.1; -.
DR   EMBL; BC033870; AAH33870.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 7
Q9N0Y0
ID   Q9N0Y0      PRELIMINARY;      PRT;   116 AA.
AC   Q9N0Y0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   VAMP-2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hippocampus;
RA   Jensen M.J., Smith L.A.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF240769; AAF64476.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 8
O35619
ID   O35619      PRELIMINARY;      PRT;   116 AA.
AC   O35619;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vesicle associated membrane protein 2.
GN   Name=Vamp2; Synonyms=mVAMP-2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Olken S.K., Doerre S., Corley R.B.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF007168; AAB62931.1; -.
DR   PIR; S35554; S35554.
DR   HSSP; Q9WUW2; 1SFC.
DR   MGD; MGI:1313277; Vamp2.
DR   GO; GO:0030141; C:secretory granule; IDA.
DR   GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR   GO; GO:0042589; C:zymogen granule membrane; IDA.
DR   GO; GO:0005516; F:calmodulin binding; IDA.
DR   GO; GO:0005543; F:phospholipid binding; IDA.
DR   GO; GO:0000149; F:SNARE binding; IDA.
DR   GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.
DR   GO; GO:0017157; P:regulation of exocytosis; IDA.
DR   GO; GO:0016083; P:synaptic vesicle fusion; IMP.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   116 AA;  12677 MW;  4E1D0D56B5409D0A CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 9
AAH02737
ID   AAH02737    PRELIMINARY;      PRT;   116 AA.
AC   AAH02737;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Vesicle-associated membrane protein 2 (Synaptobrevin 2).
GN   VAMP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002737; AAH02737.3; -.
SQ   SEQUENCE   116 AA;  12663 MW;  9CD679C4F6F1B5A8 CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 10
AAH55105
ID   AAH55105    PRELIMINARY;      PRT;   116 AA.
AC   AAH55105;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Vesicle-associated membrane protein 2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055105; AAH55105.1; -.
SQ   SEQUENCE   116 AA;  12691 MW;  4A0D0D56B5409D0A CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 11
BAC41125
ID   BAC41125    PRELIMINARY;      PRT;   116 AA.
AC   BAC41125;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   15 days embryo brain cDNA, RIKEN full-length enriched library,
DE   clone:G630012G02 product:unclassifiable, full insert sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK090178; BAC41125.1; -.
SQ   SEQUENCE   116 AA;  12691 MW;  4A0D0D56B5409D0A CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 12
Q9WUW2
ID   Q9WUW2      PRELIMINARY;      PRT;   135 AA.
AC   Q9WUW2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Vesicle associated membrane protein 2B.
GN   Name=vamp2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=99297576; PubMed=10371166;
RA   Mandic R., Lowe A.W.;
RT   "Characterization of an alternatively spliced isoform of rat vesicle
RT   associated membrane protein-2 (VAMP-2).";
RL   FEBS Lett. 451:209-213(1999).
DR   EMBL; AJ133104; CAB43509.1; -.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
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DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
SQ   SEQUENCE   135 AA;  14509 MW;  F37D14A87BDAB1F6 CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 135;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         60 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 94


RESULT 13
Q8CHR4
ID   Q8CHR4      PRELIMINARY;      PRT;   142 AA.
AC   Q8CHR4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vamp2 protein (Fragment).
GN   Name=Vamp2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA   Strausberg R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC039745; AAH39745.1; -.
DR   HSSP; Q9WUW2; 1SFC.
DR   MGD; MGI:1313277; Vamp2.
DR   GO; GO:0030141; C:secretory granule; IDA.
DR   GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR   GO; GO:0042589; C:zymogen granule membrane; IDA.
DR   GO; GO:0005516; F:calmodulin binding; IDA.
DR   GO; GO:0005543; F:phospholipid binding; IDA.
DR   GO; GO:0000149; F:SNARE binding; IDA.
DR   GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.
DR   GO; GO:0017157; P:regulation of exocytosis; IDA.
DR   GO; GO:0016083; P:synaptic vesicle fusion; IMP.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   142 AA;  15313 MW;  F1B0C9C9B495B776 CRC64;

  Query Match             81.9%;  Score 181;  DB 2;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-16;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              |||||||||||||||||||||||||||||||||||
Db         86 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 120


RESULT 14
VAM2_XENLA
ID   VAM2_XENLA     STANDARD;      PRT;   113 AA.
AC   P47193;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2)
DE   (SYBII).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang X.-H., Poo M.-M.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 32-113 FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=95324415; PubMed=7601005;
RA   Knecht A.K., Good P.J., Dawid I.B., Harland R.M.;
RT   "Dorsal-ventral patterning and differentiation of noggin-induced
RT   neural tissue in the absence of mesoderm.";
RL   Development 121:1927-1935(1995).
CC   -!- FUNCTION: Involved in the targeting and/or fusion of transport
CC       vesicles to their target membrane.
CC   -!- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC       vesicles.
CC   -!- SIMILARITY: Belongs to the synaptobrevin family.
CC   -!- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF035017; AAB88138.1; -.
DR   EMBL; U16801; AAA81376.1; -.
DR   HSSP; P19065; 1F83.
DR   InterPro; IPR001388; Synaptobrevin.
DR   Pfam; PF00957; Synaptobrevin; 1.
DR   PRINTS; PR00219; SYNAPTOBREVN.
DR   ProDom; PD001229; Synaptobrevin; 1.
DR   PROSITE; PS00417; SYNAPTOBREVIN; 1.
DR   PROSITE; PS50892; V_SNARE; 1.
KW   Acetylation; Coiled coil; Multigene family; Synapse; Synaptosome;
KW   Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     91       Cytoplasmic (Potential).
FT   TRANSMEM     92    110       Anchor for type IV membrane protein
FT                                (Potential).
FT   DOMAIN      111    113       Vesicular (Potential).
FT   MOD_RES       1      1       N-acetylserine (By similarity).
FT   DOMAIN       28     88       v-SNARE coiled-coil homology.
SQ   SEQUENCE   113 AA;  12341 MW;  6EC6C937B29BC6AB CRC64;
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Query Match 81.0%; Score 179; DB 1; Length 113;
Best Local Similarity 97.1%; Pred. No. 1.4e-15;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
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Db         57 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 91
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RESULT 15
AAH60344
ID AAH60344 PRELIMINARY; PRT; 114 AA.
AC AAH60344;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Vamp2-B-prov protein.
GN VAMP2-B-PROV.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC060344; AAH60344.1; -.
SQ SEQUENCE 114 AA; 12472 MW; AEF2EDDCDF2D1DBF CRC64;

Query Match 81.0%; Score 179; DB 2; Length 114;
Best Local Similarity 97.1%; Pred. No. 1.4e-15;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 LSELDDRADALQAGASQFETSAAKLKRKYWWKNLK 38
              ||||||||||||||||||||||||||||||||||:|
Db         58 LSELDDRADALQAGASQFETSAAKLKRKYWWKNMK 92
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Search completed: November 1, 2004, 17:59:10
Job time : 117.625 secs